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OM nucleic - nucleic search, using BW model

Run on: February 4, 2005, 11:44:23 ; Search time 636 Seconds  
(without alignments)  
10381.095 Million cell updates/sec

Title: US-10-066-521-5  
Perfect score: 4035  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	221.4	5.5	4422	US-09-388-221B-1	Sequence 1, Appl1
2	221.4	5.5	4556	US-09-388-221B-9	Sequence 9, Appl1
3	220.6	5.5	4200	US-09-388-221B-3	Sequence 3, Appl1
4	220.6	5.5	4332	US-09-388-221B-5	Sequence 5, Appl1
5	220.6	5.5	4466	US-09-388-221B-11	Sequence 11, Appl1
6	183.8	4.6	1371	US-08-910-731-1	Sequence 1, Appl1
7	183.8	4.6	1371	US-08-795-395-1	Sequence 1, Appl1
8	182.4	4.5	1386	US-08-910-731-5	Sequence 5, Appl1
9	180.8	4.5	1371	US-08-910-731-7	Sequence 7, Appl1
10	175.8	4.4	1374	US-08-910-731-3	Sequence 3, Appl1
11	175.8	4.4	1374	US-08-795-395-3	Sequence 3, Appl1
12	61	1.5	7218	US-08-232-463-14	Sequence 14, Appl1
13	60	1.5	376	US-09-023-655-395	Sequence 14581, A
14	51.4	1.3	298336	US-09-949-016-16600	Sequence 16600, A
15	50.8	1.3	64309	US-09-949-016-14581	Sequence 3209, Ap
16	47.4	1.2	4485	US-09-949-016-3209	Sequence 1, Appl1
17	47.4	1.2	4485	US-10-014-268-1	Sequence 33, Appl1
18	47.4	1.2	4486	US-10-014-268-33	Sequence 2, Appl1
19	46.6	1.2	1276	US-09-177-325-2	Sequence 2, Appl1
20	46.6	1.2	1276	US-09-411-812A-2	Sequence 2, Appl1
21	46.6	1.2	1276	US-09-590-113-2	Sequence 358, App
22	46.4	1.1	2780	US-09-620-312D-358	Sequence 14, Appl1
23	45	1.1	929	US-09-671-317-14	Sequence 14, App
24	44.8	1.1	1620	US-09-134-000C-340	Sequence 430, App
25	43.4	1.1	1001	US-09-671-317-439	Sequence 37, Appl1
26	43.2	1.1	193303	US-09-497-855A-37	Sequence 44, Appl1
27	43.2	1.1	193303	US-09-497-855A-44	

28	42.8	1.1	1449	US-09-248-796A-4693	Sequence 4693, Ap
29	42.8	1.1	767677	US-09-949-016-12147	Sequence 12147, A
30	42.8	1.1	767677	US-09-949-016-17361	Sequence 17361, A
31	42.6	1.1	693	US-09-252-991A-11050	Sequence 11050, A
32	42.6	1.1	1005	US-09-252-991A-110976	Sequence 10976, A
33	42.6	1.1	1185	US-09-252-991A-11203	Sequence 11203, A
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35	42.2	1.0	38566	US-09-949-016-15271	Sequence 15271, A
36	42.2	1.0	38566	US-09-949-016-15272	Sequence 15272, A
37	42	1.0	3117	US-09-614-221A-275	Sequence 275, App
38	41.8	1.0	7044	US-09-949-016-14113	Sequence 14113, A
39	41.6	1.0	2223	US-08-257-073-4	Sequence 4, Appl1
40	41.4	1.0	505	US-09-621-976-15639	Sequence 15639, A
41	41.2	1.0	810	US-09-614-221A-103	Sequence 103, App
42	41.2	1.0	43795	US-08-742-185-101	Sequence 101, App
43	41	1.0	505	US-09-621-976-15639	Sequence 15639, A
44	41	1.0	10391	US-09-902-540-958	Sequence 958, App
45	40.4	1.0	240157	US-09-949-016-16264	Sequence 16264, A

## ALIGNMENTS

RESULT 1									
US-09-388-221B-1									
Sequence 1, Application US/09388221B									
Patent No. 6818750									
GENERAL INFORMATION:									
APPLICANT: Reed, John C.									
TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation									
FILE REFERENCE: P-LJ 3650									
CURRENT APPLICATION NUMBER: US/09388,221B									
CURRENT FILING DATE: 1999-09-01									
NUMBER OF SEQ ID NOS: 30									
SOFTWARE: Patent In Ver. 2.0									
SEQ ID NO 1									
LENGTH: 4422									
TYPE: DNA									
ORGANISM: Homo sapiens									
FEATURE:									
NAME/KEY: CDS									
LOCATION: (1) .. (4422)									
US-09-388-221B-1									
Query Match									
Beet Local Similarity 47.9%; Pred. No. 9.1e-55;									
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;									
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QY	592	ATTGGGAATGCGCTCTAGCCAGAGATCGTGTGTCGGGCGCAAGTGTCTTAC	651						
DB	1012	ATTGGGAATGCAACCTGCGCAGGAGGTGAAGAACTGGGGAGAGCCAGCTGTAT	1071						
QY	652	CAGGAATGTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	711						
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QY	772	ATCATGTCGACAGCAAGAAAGCTGTGTTTCATTCATTCAGGTTTGTGATGACCTG	831						
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DB	1252	GTCTTGACAGAGCCGAGTTCATGAGCTGTGTGACCTGAGCCAGCCACACCGCGGAT	1311						
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Qy      1009 GTTAGAGAAATCTCCGGGAAACAAAGATCCACTTGTCTTGAACCGGGATTTGTAG 1068
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Db      2866 CTGGGCTGGA 2876
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RESULT 2
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; Sequence 9, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-I/J 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4365)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-388-221B-9
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Query Match 5.5%; Score 221.4; DB 4; Length 4556;
Best Local Similarity 47.9%; Pred. No. 9.3e-55;
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;

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Db 2506 CGTCCCTCTGAGAGACCTTGGGTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 2565  
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RESULT 3  
US-09-388-221B-3  
; Sequence 3, Application US/09388221B  
; Patent No. 6818750  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation  
; FILE REFERENCE: P-LJ 3650  
; CURRENT APPLICATION NUMBER: US/09/388,221B  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 4200  
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(4197)
US-09-388-221B-3

Query Match      5.5%; Score 220.6; DB 4; Length 4200;
Bebc Local Similarity 48.0%; Fred. No. 1.5e-54;
Matches 939; Conservative 0; Mismatches 944; Indels 72; Gaps 8;

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Qy 1192 ATTCGTGTAGCCAGAGCGGCTGTTCATCTCCATGAGTGTATGATGAGACAGAAATGG 1251
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Qy 1612 GAAAAACCTCACTGACTTTCAGAGCAACCAACCCCTGTCTTACATTACCTTGCCAG 1671
Db |||||
Qy 1249 CAGGTACCCCTCGAGGGGTGGGTCCGGGCTGTCAATCTGAAGAAAGATTGTCTCG 1308
Db |||||
Qy 1672 GCTCTCAAGCTCAGCCATTGG-----GACCCAGCTTC 1704
Db |||||
Qy 1309 AAGGCTTCTGCGGTATGCTGTGAGAGAGAGTGTGAATAGAAAGTCAAGTGTGTGATGT 1368
Db |||||
Qy 1705 AGAGACCTCTGCTCTGTGGCTGTGAGGGCATCTGGCAAAAAGAACCCCTTTTCAAGTCA 1764
Db |||||
Qy 1369 GACGACTCATGTGTTCAAGAGACTGGGAGGTGTGAGCTCCGTGCTGTGTTCACTGAAC 1428
Db |||||
Qy 1765 GATGACCTCAAGAGCATGGGTATGATGGGCGCATCATCTCACCTTCTTGAAGATGGGT 1824
Db |||||
Qy 1429 ATCTCTTCCCAAGACGACCATGTGAGAGATACATACCTTCTTCCAGCTGCTCCAG 1488
Db |||||
Qy 1825 A---TTCTTCAAGAGCAACCCATCCCTCTGTAGCTACAGCTTCATTCACCTCTGTTCAA 1881
Db |||||
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Qy 1489 GACTTGTGCGCGCTTGTATACGTGTGAGGGGCTTGAAATCGACGCTCTGTC 1548
Db |||||
Qy 1882 GAGTTCCTTGTGAGCAAGTCTCTATGTCTTGAGAGATGAGAGGGAGATTAACATTC 1941
Db |||||
Qy 1549 CCTCTGACGTGAGAGAACAAAGAGGTCATGAGAGCTTAAACAGGAGCTTCATATC 1608
Db |||||
Qy 1942 AATTGCATCATATGTTTGAAGAAACCTTGAAACATATGATATACATGAGCTTTGGG 2001
Db |||||
Qy 1609 CACTGCTTGTGATGAAGCGTTTCTTGTGTGGCTCTGTGACGGAAGCGTAAGAGGCCA 1668
Db |||||
Qy 2002 GCATC-----AACCAACGTTTCTATGTGGGCTGTAAAGTATGAGGGGAGAGAGAG 2055
Db |||||
Qy 1669 CTGAGGCTCTGCTGGGCTGTCCCGTTCCCTCGGGGTGAAGCAAGAGCTTGTCACTGG 1728
Db |||||
Qy 2056 ATGAGAGAACTCTTCACTGCGGCTGTCTCAAGGGGAGAACTGATGACAGTGGTCCG 2115
Db |||||
Qy 1729 GTCTCTGTTGGGTGACGAGCCCTAATGCCAACCCAGAGAGACCTGGAAGCGCTTC 1788
Db |||||
Qy 2116 TCCTGAGCTGTGCTGCAAGCC-----ACACTCTGTGAGTCCCTC 2157
Db |||||
Qy 1789 CACTGTCTTTCAGACTCAAGACAAAGATTGTGCTGTGGCATTTAAACGCTTCCA 1848
Db |||||
Qy 2158 CACTGTCTGTACAGACTTCGGAACAAACGTTCCCTGACACAAATGATGAGGCCCATTTGAA 2217
Db |||||
Qy 1849 GAAGTGGCTTCCGATTAAACAGAACCTGGACTTATATGATTTCTTCTGCTCCAG 1908
Db |||||
Qy 2218 GAAATGGGCAATGTGTGTGAAGAACAGATGAGCTCTTAATGTGTACATTTCTGCAATTA 2277
Db |||||
Qy 1909 CACTGTCCGATTTTGGGAAATTTGGGTGATGTCAAAAGGAACTTCCCAAGATGAG 1968
Db |||||
Qy 2278 TTCAGCCGCACTGTAAAGAGCTTCAGCTAATTAAGGACAG-----CAGCACAATC 2330
Db |||||
Qy 1969 TCCGCTGAGGAGATCTCTGTGTGCTCTTATGATGTCGGGATTAAGACCTCATTTAGAGAG 2028
Db |||||
Qy 2231 AAGATGAGGCCACCATGTGATGTCCTGTCAAGGTGG-----TCCAGTCAAGATGCC 2385
Db |||||
Qy 2029 CAGTGGAAATTTCTGCTCATGCTTGGGACCAACCACTGCGGACGCTGAGACTTG 2088
Db |||||
Qy 2386 TATTGGAGATTCCTTCTCCGCTCTCAAGTCAACCAAACTGGAAGAGCTGGAACCTTA 2445
Db |||||
Qy 2089 GGACGAGCATCTCGACAGAGCGGGCCATGAAGCCCTGTGTGCAAGCTGAGGCACTCC 2148
Db |||||
Qy 2446 AGTGAATCTGCGAGCCACTGTGACGTAAAGATTTTGTAAAGACCTGAGAGCGCCCT 2505
Db |||||
Qy 2149 ACCTGCAAGATACAGACCTGATGTT---TAGAAATGACAGATTAACCTCTGTGTGAG 2205
Db |||||
Qy 2506 CGTGCCTCTGAGAGACCTGTGGGTTGGCTGTGGCTGTGACAGCTGAGAGACTGCAAG 2565
Db |||||
Qy 2206 CACTCTGAGAAATCTGATGAGCCAACTGTAACCTTAAGATCCTCAACTTGGAGGAC 2265
Db |||||
Qy 2566 GACCTTGCCTTGGGCTGAGAGGCCAACAGACCTGACCGAGCTGAGACTGAGCTTCAAT 2625
Db |||||
Qy 2266 CACTGGAAGAAAGAGATGTAAGATGGCGGTGGAACCTTAAACCCCAAAATGTTTG 2325
Db |||||
Qy 2626 GTGCTACGAGATGTGAGGCCAAACACTTTGCAAGAGACTGAGACGCCAGGTGCAAG 2685
Db |||||
Qy 2326 TTGAGTCTTGAAGGCTGATATGCTGTGATGATGACCATGCTGTATCTGAAGATCTCC 2385
Db |||||
Qy 2746 TCTGTCTTATGTGCAAGCCCAAGGCTGAAGAGCTAAGCTGCGACGAAACAACTGGAAT 2805
Db |||||
Qy 2446 GACCAAGGAGTAATGCTCTCAATGATGCTTGAAG 2480
Db |||||
Qy 2806 GACGTTGGCGTGCAGCTGTGTGAGGGGCTCAG 2840
Db |||||
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RESULT 4  
US-09-388-221B-5  
; Sequence 5, Application US/09388221B



Patent No. 6818750  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
TITLE OR INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation  
FILE REFERENCES: P-LJ 3650  
CURRENT APPLICATION NUMBER: US/09/388,221B  
CURRENT FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 4332  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (1)..(4332)  
US-09-388-221B-5

Query Match 5.5%; Score 220.6; DB 4; Length 4332;  
Best Local Similarity 48.0%; Pred. No. 1.6e-54;  
Matches 939; Conservative 0; Mismatches 944; Indels 72; Gaps 8;  
QY 532 TTGATTCAGACCGGTGGGCTTCCGGCTTCGACGGTGTTCGACGGAAGTCAGGA 591  
DB TTTGGCCAGGCTGATACCAAGAACTCGCATATGATACAGGGGGCTGTGGA 1011  
QY 592 ATTGGGAATGGCTTACGCAAGAAAGATCGTGTCTGTGGGGCGAAGTGAATCTAC 651  
DB 1012 ATTGGGAAGTCAGACCTGGCAGGAGGTGAAGAGCTGGGGAGAGGCGAGCTGTAT 1071  
QY 652 CAGGAATGTTCTCTAGTCTTCTCTCCCGTTAGAGATGACGGAAGAAAGAG 711  
DB 1072 GGGGACGGCTTCAGCATGTCTTCTACTTCAGCTGAGAGAGCTGGCCATCCAGTGG 1131  
QY 712 AGCAGTGCACAGATTCATCTCAAGGAGTGGCCAGCTCCAGGCTCCGATGAGAG 771  
DB 1132 GTGAGTCTCGGTGAGCTCATCGAAAGATGGAGACGACATCCGGCTCCCATTAAGAC 1191  
QY 772 ATCATGTCCGACCAAGAAAGCTGTGTTCATCATTAAGCGTTTCGATGACTGGGCTCT 831  
DB 1192 ATCTGTCTAGGCGCAGAGCGGCTGTCTTCATCTCCAGATGTGATGAGACAGAGATGG 1251  
QY 832 GTCCCAACAAATGACA---CAAGCTCTGCAAGAGCTGGGCTGAGAACAGCTCCGTTCC 888  
DB 1252 GTCTTCGAGAGCGGAGTTCGAGCTGTGTCTGCACTGAGACCAAGCCAGCCGAGAT 1311  
QY 889 ACCCTCATACGACAGTCTGCTGAGAGAGTCTGTCTCCCTGAGTCTCTTCATGCTCAC 948  
DB 1312 GCATGTGCTGGGCGAGTTGTGGGAAAATTAATTAATTCCTCCGAGGATCTTCTGATCAG 1371  
QY 949 GTCAAGACGTGGGACAGAGAGTCAAGTCAAGTGTGTCTCCCGTTAATCTGTTA 1008  
DB 1372 GCTGGGACCAAGCTCTGCAAGACTCATCTCTTTGGAGAGGCAAGTTGGGATAGAG 1431  
QY 1009 GTTAGAGGATCTCCGGGGAACAAGATCACTTGTCTCTGAGCGGGGATTTGTAG 1068  
DB 1432 GTCTGGGGTCTCTGAGTTCAGCAGAGGAAGATTTTCTACAGATATTTCACAGATAA 1491  
QY 1069 CATCAGAAACACAGAGGTGCTGTCGATCATGAACAACGTCGAGCTGTCAGACAGTGC 1128  
DB 1492 AGGCAAGAAATTAGAGCTTTAGTGTCTAAATCAAAAGAGCTGTGGGCCCTGTGT 1551  
QY 1129 CAGTGTCCCGCGGTGGCTCTCTCATCTGCTGCGCTTCAGCTGACAGAGAGTGTGGGG 1188  
DB 1552 CTGTGTGCTGGGTGTCTGTGCTGGCTGCACTTGTCTGATGACAGCAATGAAAGGGAG 1611  
QY 1189 GAGAGCGTGGCCCTTCAACCAACGCTCAAGGCTCGACGGCGCTTTTGTGTTAT 1248  
DB 1612 GAAGAACTCAGACTTCACAGACCAACCAACCTCTGTCTACATTAATTCCTGAG 1671  
QY 1249 CAGCTCACCCCTCGAGGCGGTGCTGGCGCTGTCTCATCTGAGAAAGATGTCTCTG 1308  
DB 1672 GCTCTCAGAGCTCAGGCAATGG-----GACCCAGCTC 1704

QY 1309 AAGCGTCTCCCGTATAGGCTGTGAGGAGAGTGTGAATAGAAATCAGTGTGATG 1368  
DB 1705 AGAAGCTCTCTCTCTCTGCTGTGAGGGGATCTGGCAAAAAGAACCTTTTCACTGCA 1764  
QY 1369 GACCACTCATGTGTTCAAGAGCTGGGAGAGTGTGAGCTCCGTCTCTTTCACTGAC 1428  
DB 1765 GATGACCTCAGAGAGCATGTGGGTAGATGGGCGCATCATCTCCACCTTCTTAAGATGG 1824  
QY 1429 ATCTTCTCCCAAGACGACATGTGAGAGATCATACCTTCTCCACCTCAGTCTCAG 1488  
DB 1825 A---TCTTCAAGAGCACCCCATCTCTGAGTACAGCTTCATTCACCTTGTTCAA 1881  
QY 1489 GACTTGTGCGCGCTTGTATAGTGTAGAGGCGCTGAAATACAGCCAGCTCTCTGC 1548  
DB 1882 GAGTCTTTGACAGAAATGTCTTATGTCTTGAAGATGAGAAAGGAGAGTAAATCTT 1941  
QY 1549 CCTCTGATCGTTGAGAAACAAAGAGTTCATGAGCTTAAACAGGAGCTTCCATATC 1608  
DB 1942 AATTGATCATATGATTTGAAAAGACGCTAGAGCATATGGAATATACATGCTGTTGG 2001  
QY 1609 CACTGCTTTGATGAAAGCTTTCTTGTGCTCTCGAGCGAAGAGCTTAAGAGGCA 1668  
DB 2002 GCATC-----AACCAACGTTTCTTATGTGGCGCTGTTAAGTGTAGAGGGGAGAGAG 2055  
QY 1669 CTGAGAGCTGCTGGGCTGTCCCGTCCCTGGGGGGTGAAGAGAGCTTCTGCACTGG 1728  
DB 2056 ATGAGAAACATCTTTCATCTCCGCTGTCTAGGGAGAGAACTGATGATGTGCTCCG 2115  
QY 1729 GTCTCTGTGAGGTGACAGAGCTTAAATGCAACCCAGAGAGACCTTGAAGCTTC 1788  
DB 2116 TCCCTGAGAGCTGCTGAGAGC-----ACACTCTGAGAGCTTC 2157  
QY 1789 CACTGTCTTTTGGAGTCAAGACAAAGATTTGTGCTTGGCATTAACAGCTTCCAA 1848  
DB 2158 CACTGTGTGACGAGTCTCGAACAACAGTCTTCAACAAGATGAGCCATTTGAA 2217  
QY 1849 GAAGTGTGGCTTCGATTAACAGAACCTGACCTTGAATGATCTTCTGCTGCTCAG 1908  
DB 2218 GAATGTGGCATGTGTGTAAGAAACAGATGAGACTTTAGTGTGCACTTTTGTGATTA 2277  
QY 1909 CACTGTCCGATTTTGGGAAATTCGGGTGATGTCAAGAGATCTTCCAAAGATGAG 1968  
DB 2278 TTCAGCGGCCACGTAAGAGCTTCAAGTATTAAGGGCAG-----CAGCACAGATC 2330  
QY 1969 TCCGCTAGGATGCTCTGTGTCTCTATGATGCGGGATTAAGACCTTATGAGAG 2028  
DB 2331 AACATGAGGCCCAACATGTGATGCTGTTCAGGTGG-----TCCAGTCAAGATGCC 2385  
QY 2029 CAGTGGGAAGTTTCTGTCCATGCTTGGACCAACCAACGACCTGGGAGCTGGAGCTG 2088  
DB 2386 TATTTGGAGATTTCTTCTCTCTCTCAAGGTTCACAGAAACCTGAAAGAGCTGAACTTA 2445  
QY 2089 GGCAGACAGATCTGACAGAGCGGGCATGAAGACCTGTGTGCAAGCTGAGGATGCC 2148  
DB 2446 AGTGAAGACTGTGAGGCACTGTGAGTGAAGTCTTTTGAAGCCCTTAAGAGCGCCT 2505  
QY 2149 ACTGCAAGATACAGACCTTGATGTT---TGAATGACAGATTAACCTGTGTGAG 2205  
DB 2506 CGTGTCTCTCGAGAGACCTGCGGTGGCTGTGTGCTGAGCTGAGAGAGCTGCAAG 2565  
QY 2206 CACTGTGAGAAATCGTCATGTGACCAACGTAAACCTTAAGATCCCTCAACTTGGAGGACC 2265  
DB 2566 GACCTTGTCTTGGCTGTGAGAGCCACCAAGACCTTGAACGAGCTGAGACCTTAAT 2625  
QY 2266 CACTGAAGAGAGAGATGTAAAGATGGCGTGTGAACCTTAAACACCAAAATGTTTG 2325  
DB 2626 GTGCTCAGAGATGTGTGAGGCAACACCTTTGCCAGAGCTGAGACGCGAGCTGAG 2685  
QY 2326 TTGAGTCTTTGAGGCTGATGTGCTGTGATTAACCAATGCTGTAACTGAAAGATCTCC 2385  
DB 2686 CTACAGGAGCTGAGAGCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGAGAGCTGAGCC 2745

QY CAAATCCCTACGACCTCCCCGAGCTGTAATCTCTGAGCTCGGCGAGGAAATAAGTGCAG 2445  
 2386  
 Db TCTGTGCTTAGTGCAGCCGCCACGCTGAAAGAGACGTAACGCTCGCAGCGAGAACTTCCCTGAT 2805  
 2746  
 QY GACCAGGGAGTAATGCTCTCTCAGTGATGAGCTTTGAG 2480  
 2446  
 2806 GACGTTGGCGTGCAGACTGCTCTGTGAGAGGGGCTCAG 2840

## RESULT 5

```

US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-IJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4272)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-388-221B-11

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Query Match	5.5%	Score 220.6	DB 4	Length 4466
Beet Local Similarity	48.0%	Fred. No. 1.6e-54		
Matches 939	Conservative	0	Mismatches 944	Indels 72
				Gaps 8
Qy	532	TTTGATTTAGACCGGCTGGGGCTTCGCGGCTCGACGGGTGTTTTCGACGGAAAGTCAGGA	591	
Db	952	TTTGGCCAGGCGCTGGATATCCAGAAAGCTGCGATATCTGACAGGGGGCTGTGGA	1011	
Qy	592	ATTGGGAATCGGCTTATGACCAAGAAAGATCGTGTGTGGCGCAAGGTGACTTAC	651	
Db	1012	ATTGGGAAGTCAACACTGGCCAGGCGAGGTGAAGAAAGCTGGGGAGAGGCCACTGTAT	1071	
Qy	652	CAGGGAATGTTTCTCTTAAGTCTTCTTCTCTCCCGTTAGAGAGATGACGGGAAGAAGAG	711	
Db	1072	GGGAGCCGCTTCCAGCATGTCTTCTTACTTCACTTCAGCTGACAGAGCTGGGCCCAATCCAAAGTGT	1131	
Qy	712	AGCAGTGTCAAGAGTTTATCTCCAGGGAGTGGGCAAGTCCCAAGGCTCCGGTACGGAG	771	
Db	1132	GTGAGTCTTCGCTGAGCTATATCGAAGAAAGATGGAGACGCCACTCCGGCTTCCATTAGACAG	1191	
Qy	772	ATCATGTGCCAGCCAGAAAGGCTGTGTTTCATCTTACATTCGATTCGATTCCTGGGCTCT	831	
Db	1192	ATTCGTGTAGGCCAGAGCGGCTGTCTTCAATCTCGATGTGTATGATGACCGAGATGG	1251	
Qy	832	GTCTCTCAACATGACA---CAAAGCTTCGAAAGATGCTGGGCTGAGAGACGCTCCGTTT	888	
Db	1252	GTCTTTCAGAGCCGAGTTTCTGAAGTCTGTGTGTGACCTGGAGCCAGCCAGCCCGCGGAT	1311	
Qy	889	ACCCTCATACGACAGTCTGCTGAGGAAGGTCGAGCTCCCTGAGTCCCTTCATAGSTCAAC	948	
Db	1312	GCACTGCTGGGGAATTTTCTGTGGGGAACATATCTTCCGAGGCACTTCTTCTATACG	1371	
Qy	949	GTCAAGACGTGGGCAAGAAAGCTCAAGTCAGAGGTCTGTCTCCCGTTACTCTGTA	1008	
Db	1372	GCTGGACCAAGGCTGTGACAACTCATTTCTCTTTGGAGCAGGACGTTGGGTAGAG	1431	
Qy	1009	GTTAGAGGAATCTCCGGGGAACAAAGATTCATCTTGTCTCTTTGAGCGCGGATTTGGTAG	1068	
Db	1432	GTCTCTGGGTTTCTGAGTCCAGCAGGAAGGAATATTTCTACAGATATTTTCACAGATGA	1491	

QY	1069	CATCAAGAAACACACAGGGTTCGCTGCATCATGAACAACCTGAGCTGCTGCACATC	1128
Db	1492	AGGCAGACCAATTAGAGCCTTTAAGTTGGTGCATTAATCAAAACAAGAGCTCTGGGCTCTGT	1551
QY	1129	CAGGTCGCCCGCGAGGGCTCTCATCTGCGTGGCCCTGCAGCTGCAGAGAGTGTGGGG	1188
Db	1552	CTTGTGCTCCCTGGGTGTCTGTGCTTGGCTTGCACCTTGCTGATGCAGAGTAGAGCGAAG	1611
QY	1189	GAGAGCGTGGCCCCCTTCAACCAACAGCTCAAGGCTGCACGCGCTTTGTGTTTCAT	1248
Db	1612	GAAAACTCACTGACTTCCAAAGACCAACCAACCTCTGTGTACATTAACCTTGCCACG	1671
QY	1249	CAGCTCACCCCTCGAGGGCGTGTCCGGCGCTGTCTCAATCTGAGGAAAGATTGTCTG	1308
Db	1672	GCTCTCCAGAGCTACGACCATGG-----GACCCCAAGCTC	1704
QY	1309	AAGGCGTTCTGCGCATAGCTGTGAGAGGAGTGTGAATAGGAAGTCAGTGTTGATGCT	1368
Db	1705	AGAGACCTCTGCTCTTGGCTTGGAGGGGATCTGGCAAAAAGAACCTTTTCAGTCCA	1764
QY	1369	GACGACCTCATGTTCAAGAGACTCGGGGAGTCTGAGCTCGGTCTGTTCATGATGAAC	1428
Db	1765	GATGACCTCGAGGAAGCANTGGTTAGATGGGCCCATCATCTCCACTTCTTGAAATGGGT	1824
QY	1429	ATCCTTCTCCAGACAGCCACTGTGAGAGATCTACACTTCTTCCACTCAGTCTCCAG	1488
Db	1825	A---TTCCTTCAAGAGACACCCCATCCCTGTGAGCTTACAGCTTCATTCACCTCTGTTTCAA	1881
QY	1489	GACTTCTGTGCGCGCTTGTACTAGTGTGAGGGCGCTGGAAATCGAGCCAGCTCTCGC	1548
Db	1882	GAGTTCCTTGGAGCAATGTCTTAAGTCTTGAGAGATGAGAGGGAGAGGTAACATTCT	1941
QY	1549	CCTCTGTACGTTGAGAAAGACAAAGAGGTCCATGAGCTTAAACAGGAGCTTCCATATC	1608
Db	1942	AATTGCAATCAATGATTTGGAAAACCGCTAGAAACATATGGAATACATGGCTGTTGGG	2001
QY	1609	CACTCGCTTGGATGAAGCGTTTCTTGTGGCTCTGTGAGCGAAGCTGAGAGGCCA	1668
Db	2002	GCATC-----AACCAACAGTTTCTTATGTGGGCTGTGTAAGTATGAGGGGAGAGAG	2055
QY	1669	CTGGAAGTCTGCTGGGCTGTCCCGTTCCTCGGGGGTGAAGCAAGCTTCTGCACCTGG	1728
Db	2056	ATGGAAGAACATCTTTCACCTGCGGCTGTCTCAGGGGAGAGAACCTGAATGAGTGGTCCG	2115
QY	1729	GTCTCTGTGTTGGGTCAAGAGCTTAATGSCACACCCAGAGAGACACCTTGAGCGCTTC	1788
Db	2116	TCCTCGACAGCTGCTGCTGCAGC-----ACACTCTGTGAGATCCCTC	2157
QY	1789	CACGTCTCTTTCGAGACTCAAGACAAAGATTGTGCTTGCGCATTTAAACGCTTCAA	1848
Db	2158	CACGTCTGTATCGAGACTCGGAAACAAACGTTCTGACACAAAGATAGGCCATTTGAA	2217
QY	1849	GAAGTGTGACTCCGATTTAACAGAACTGGACTTGATAGCATTTCTTGTGCTCCAG	1908
Db	2218	GAAATGGGCAATGTGTGAGAAACAGACATGAGCTCTTAAGTGCACATTTCTGCATTAAA	2277
QY	1909	CACGTCCGTAATTTGCGGAAAAATTCGGGTGAGTGTCAAAAGGAGCTTCCCAAGATGAG	1968
Db	2278	TTCAAGCGGCACGTGAAGAAAGCTTCAAGCTGATTTAGGGCAGG-----CAGCACATATC	2330
QY	1969	TCGCTAGAGGATGCTCTGTGGTCCCTCTATGATGCGGAGTAAAGACCTCATTTAGAGAG	2028
Db	2331	AAACATGGAGCCCAACATGGTATGTCGTTCAGGTGG-----TCCAGTCAACAGATGCC	2385
QY	2029	CAGTGGGAGATTTCTGTCTCAATCTTGGACACCAACCAACTCTGGCGCAGCTGGACCTG	2088
Db	2386	TATTTGGAGATTCCTTCTCCGTCTCAAGGTCAACGAAACCTGAAGAGAGCTGACCTTA	2445
QY	2089	GGCAGCAGCATCTCGACAGAGCGGGCCATGTAAGCCGTGTGCTCAAGCTGAGGCATCCC	2148
Db	2446	AGTGAAGAACTCGCTGAGCCACTCTGCAGTAAAGGTCTTTGTATGAACCTCTGAGAGCGCCT	2505
QY	2149	ACCTGCAAGATACAGACCTGATGTT---TAGAATGACAGATTAACCTCTGTGTGACG	2205

Db	2506	CGCTGCTCTCTGGAGACCTCTGGCTGGCTGCTGTGTGCTCTCAAGCTGAAGACTGCAG	2565
Qy	2206	CACCTCTGGAGATGTCATGTGCGCCAAACGTAACTTAAGATCCCTCACTTGGAGGCACC	2265
Db	2566	GACCTTGCTCTTGGGCTGAGAGCCAAACGAGACCTGAGCCGAGCTGGACTAGCTTCAAT	2625
Qy	2266	CACCTGAAGAAAGAGATGTAAAGATGGCGCTGTGAAGCTTTAAACACCCAAAATGTTTG	2325
Db	2626	GTGCTCAAGGATGCTGGAGCCAAACACTTTTGCAGAGACTGAAGACACCCTGCGCAG	2685
Qy	2326	TTGGAGCTCTTGAAGGCTGATTTGCTGTGAATGACCAATGCTGTAACTTGAGATCTCC	2385
Db	2686	CTACAGGCACCTGCACTGTGTCAAGCTGTGTGCTCTCAAGTGTACTGTGTGCGAAGACTGCC	2745
Qy	2386	CAAAATCTTACGACCTCTCCCGACGCTGAAATCTCTGAGCCTGGCAGAAACAAGTGA	2445
Db	2746	TCTGTGCTTAATGCGCAGGCCCGACCTGAAGAGAGCTAGACCTGCAGAGAAACAACCTGAT	2805
Qy	2446	GACCAAGGAGTAATGCTCTGAGATGATCCCTTGAG	2480
Db	2806	GACGTGGCGTGCACTGCTCTGTGAGGGGCTCAG	2840

RESULT 6  
 Sequence 1, Application US/08910731  
 Patent No. 5932440  
 GENERAL INFORMATION:  
 APPLICANT: CHATTERJEE, DEB K.  
 APPLICANT: SHANDILYA, HARINI  
 TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVE., N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,731  
 FILING DATE: (herewith)  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/795,395  
 FILING DATE: 04-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/794,546  
 FILING DATE: 03-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/024,057  
 FILING DATE: 16-AUG-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ESMOND, ROBERT W.  
 REGISTRATION NUMBER: 32,893  
 REFERENCE/DOCKET NUMBER: 0942.3440003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1371 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:

NAME/KEY:	CDS	LOCATIONS:	1..1368
us-08-910-731-1			
Query Match	4.6%	Score 183.8	DB 2; Length 1371;
Best Local Similarity	47.2%	Pred. No. 76-44;	
Matches 591; Conservative	0;	Mismatches 657;	Indels 3; Gaps 1;
2016	CCTGATTTAGGAGCAGTGGGAAAGATTTCTGCTCATGCTTTGGCA	CCCA	CCCACTTGGC
102	CCTCAGCGAGGAGCAGTGGAAAGCATCGTTCTGCTCCCGGCGCA	ACCCCTCCCTGAC	161
2076	GCAGCTGGACCTGGGCGACGACATCTCTGACAGAGCGGGCCAT	TAAGAACCTCTGTGCCAA	2135
162	CGAGCTCTGCTTCGCGACCAACGAGCTGGGGGAAGCCGGCGT	GACCTGTGCTGCGAAG	221
2136	GCTAGGCGATCCACCTGCAAGATACAGACCTCATGTTTGAAT	GACACAGATTAACC	2194
222	CTTCAGAGGCCCACTTGCAGATCCAGAAAGCTCAGACCTGCA	GAATCTCTCCCTGCGA	281
2195	--CTGTGTGTCAGACACTTGGAGATTCATGCGCAACCGTAA	ACTTAAGATCCCTCAA	2252
282	GGGGGGCTGGGGGGTCCGCGCCAGACAGCTGCGCTCCCTG	CCACGCTGCGGAGCTGCA	341
2253	CTTGGAGAGCCACCACTGAAAGAAAGATGTAAAGTGCCTGT	GAAGCTTAAACA	2312
342	TCTCAGCGACACCCACTGGGGGAGCGCGGCTGCGCTGTCT	GTATGAGGGGCTCTGGA	401
2313	CCGAAATGTTTGTGTGAGTCTTTGAGGCTGGAATGTGCTGT	GGATTGACCCATGCTCTTA	2372
402	CCCCAGTGCACCTTGAAGAACTGCAGTTGGAATCTGCGCT	GTACGCGCCGACAGCTG	461
2373	CCTGAGATCTCCCAATTCCTTACGACTCCCGACGCTGAAT	CTCTGTAGCCTTGGAGG	2432
462	CGAGCCCTGGCTCTGGGTGCTCAGGGGACAGCGGGGCTT	GAAGAGCTCAGCGTGAACA	521
2433	AAACAGGTGACAGACAGAGGATTAATGCTCTCAGTGAAT	GCCTTGTGAAGTCTCCACGT	2492
522	CAACGATCGGCGAGGCGCGCGCGCGGTCTGGGCAAGGT	CTGTGACACTGTGCTG	581
2493	CGCCCTGACAAAGCTGATATCTGAGAGCTGTGGCATCA	AGCCACCGGTTGCCAGATCT	2552
582	CGAGCTGAGACGCTCAGCTGAGAACTGGGTCTACACG	CACCACTGCAAAAGACT	641
2553	GGCTCAGCCCTCGTACAGCAACCGGACCTTGAACA	CACTGTATCCAACAAGCTT	2612
642	GTGGGAAATTTGGCTTCCAGAGCTCGCTGAGGGA	ACTTGAACCTGGGACGAACGGGCT	701
2613	GGGAGCAAGAGGTAAATCTACTGTGTGCATGAGGCTT	CCCACTGTATCTTGA	2672
702	GGGCGAGCGGGGCAATACCGAGCTGTGCCCGGGCTCT	TGTAGCCCGCTCCGCTCAA	761
2673	GAGGCTGATCTGAATCAGTGGCCACTTGGACA	ACGGCTGGCTGTGGTTTTCTTGTGAC	2732
762	GACCTGTGTGCTCGGAGGTGTGACATCACCGC	ACAGTGGCTGACAGACCTTGGCGGT	821
2733	GCTTATGGGTAACTCATGTGCTGACGACCTTGAAG	CTTGAAGCAAA	2792
822	CTTCCAGGCCAAGAGAACCTTGAAGAGCTCAGTCT	GGCGGCAACAAGCTGGCGAGGA	881
2793	TGGCGTGAAGCTTCTGTGCGAGGTCATGAGAA	CAACTTGTCTATCCAGACTTGA	2852
882	GGGGCGCCGGCTGTGTGCGAGAGCTGTGCA	CGCCGGCTGCGAGCTGGAGTCCCTGTG	941
2853	GTTTGTAAAGTTCATCTCACCGCGCGGTCTGTGA	AGTCTGTCTGTGTATCTGAG	2912
942	GGTAAAGTCTTCAGAGCTTCAACGGGCGCTGTG	CAGACGTCATGATGCTGACCA	1001
2913	GAGCAGACACTTGAAGAGCTGTGATCTCA	CGGACAAATGCTCGGTGTACAGGTGGGTTGC	2972
1002	GAAACAGACTCTCTGTGAATCTTCAATTGAGCAG	CAACAACTGGGTATCTTGGCATCA	1061
2973	TGCGCTGTGCGAGGACTGAAGCAAAAGAA	CATGTTTCTGACAGACTCGGGTTGAAGC	3032



Dh 1182 CTGGAGAGCTGAGCTGAGCAACACTGTGTGGCGACCCGGCGTCTGACCTGCT 1241  
Qy 3153 TTGGCCTTTGGCTGTCCAGCTTAACATTAATTTGGGCTGTGGAAATGGCAGTA 3212  
Db 1242 GGGGAGCTTGAGAGCAGCCGGGCTGGCCCTGAGAGCAGCTGTCTGTACGACCTACTG 1301  
Qy 3213 CCCTGTGCAATTAAGAAAGCTGTGAGAAAGTGAAGTCACTACAGCCCG 3263  
Db 1302 GACGAGAGAGGTGAGAGACCGCTGACAGGCCCTGAGGGGAGCAAGCCCG 1352

## RESULT 8

US-08-910-731-5  
Sequence 5, Application US/08910731  
Patent No. 5932440

## GENERAL INFORMATION:

APPLICANT: CHATTERJEE, DEB K.

APPLICANT: SHANDILYA, HARINI

TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., N.W., SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,731

FILING DATE: (Herein)

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/795,395

FILING DATE: 04-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/794,546

FILING DATE: 03-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/024,057

FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0942,3440003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1386 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

US-08-910-731-5

Query Match 4.5%; Score 182.4; DB 2; Length 1386;

Best Local Similarity 47.1%; Pred. No. 1.9e-43;

Matches 595; Conservative 0; Mismatches 666; Indels 3; Gaps 1;

Qy 2000 GGATGGCGGATTAAGACCTCTATTGAGAGAGAGTGGGAAGATTCTGCTCAATGCTTGGCA 2059  
Db 101 GGCTGAGAGACTGTGGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 160  
Qy 2060 CCACACCAACCTGCGGAGCTGAGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2119  
Db 161 TCAACCTGCACTGGAG 220

Qy 2120 AGACCTGTGTGCCAAGCTGAGGATCCACCTGAGAGATACAGACCTGATGTTTAA 2179  
Db 221 ATTGGTCTCCAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 280  
Qy 2180 ATGACACATTAACC--CTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2236  
Db 281 ACTGTGCTGAG 340  
Qy 2237 ACCTAAGATCCCTCAATCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2296  
Db 341 CCTGAG 400  
Qy 2297 GTGAGAGCTTAAACACCCAAATGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2356  
Db 401 GGAAG 460  
Qy 2357 TGAACCATGCTGTGAG 2416  
Db 461 TCTGGCTGAG 520  
Qy 2417 CTGAGAGCTGAG 2476  
Db 521 AGCTACAGTTAG 580  
Qy 2477 TGAAGAGCTCCAG 2536  
Db 581 TGAAG 640  
Qy 2537 CGGGTGGAG 2596  
Db 641 ACAAGTGGAG 700  
Qy 2597 TATCCAAAG 2656  
Db 701 TGGGAG 760  
Qy 2657 CCACAGTGTGAG 2716  
Db 761 CCAAGTCCAG 820  
Qy 2717 GTTTCTTGTGAG 2776  
Db 821 GGGATCTGTGAG 880  
Qy 2777 ACCCTGAG 2836  
Db 881 ACGAGCTGGAG 940  
Qy 2837 ATTCACAG 2896  
Db 941 AGCTGAG 1000  
Qy 2897 CCTGTGTGATCTGAG 2956  
Db 1001 GCTCAGTGTGAG 1060  
Qy 2957 GTGACGAG 3016  
Db 1061 AGGATGCGGAG 1120  
Qy 3017 GACTCGGAGTGAAG 3076  
Db 1121 TGTCTGTGTGAG 1180  
Qy 3077 TTTCTGAG 3136  
Db 1181 TGTGAG 1240  
Qy 3137 GAATGATAG 3196  
Db 1241 GCATTCCTGAG 1300  
Qy 3197 TGTGGAATGAG 3256

Db 1301 TGTACGATTACTGTCTGATGAGAGACCGGCTGAGGCTCTGAGAAAGACA 1360  
QY 3257 AGCC 3260  
Db 1361 AGCC 1364

## RESULT 9

US-08-910-731-7  
Sequence 7, Application US/08910731  
Patent No. 5932440

GENERAL INFORMATION:

APPLICANT: CHATTERJEE, DEB K.

APPLICANT: SHANDILYA, HARINI

TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., N.W., SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,731

FILING DATE: (Herewith)

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/795,395

FILING DATE: 04-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/794,546

FILING DATE: 03-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/024,057

FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0942, 3440003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1371 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: CDNA

US-08-910-731-7

Query March 4.5%; Score 180.8; DB 2; Length 1371;

Best Local Similarity 47.1%; Pred. No. 5.5e-43;

Matches 588; Conservative 0; Mismatches 657; Indels 3; Gaps 1;

QY 2016 CCTGATTGAGAGAGATGGAGAAATTTCTGCTCCATGCTTGAGACCCACCCACCTGCG 2075

Db 102 CCTCAGGAG 161

QY 2076 GCAAGCTGAG 2135

Db 162 GCAAGCTGAG 221

QY 2136 GCTGAGAGATCCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2194

Db 222 CTTGAG 281

QY 2195 --CTGTGTGAG 2252

Db 282 GCGCGGCTGCGGAG 341

QY 2253 CTTGAG 2312

Db 342 TCTCAGGAG 401

QY 2313 CCCAAATGTTGTTGAG 2372

Db 402 CCCCAGGAG 461

QY 2373 CTTGAGAGATCTCCAAATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2432

Db 462 GAG 521

QY 2433 AAAG 2492

Db 522 CAAG 581

QY 2493 CGCCCTGAG 2552

Db 582 CCAAG 641

QY 2553 GAGCTGAG 2612

Db 642 GTGCGAG 701

QY 2613 GGGAG 2672

Db 702 GGGAG 761

QY 2673 GAGGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2732

Db 762 GACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821

QY 2733 GCTTATGAG 2792

Db 822 CTTGAG 881

QY 2793 TGGGCTGAG 2852

Db 882 GGGGCTGAG 941

QY 2853 GTTGTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2912

Db 942 GGTGAG 1001

QY 2913 GAGCAG 2972

Db 1002 GAAAG 1061

QY 2973 TGGGCTGAG 3032

Db 1062 GAG 1121

QY 3033 ATGTGAG 3092

Db 1122 CTGAG 1181

QY 3093 TCTGAG 3152

Db 1182 CTTGAG 1241

QY 3153 TTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTT 3212

Db 1242 GAG 1301

QY 3213 CCGTGTGAG 3260

Db 1302 GTTGTGAG 1349

RESULT 10  
US-08-910-731-3  
; Sequence 3, Application US/08910731  
; Patent No. 5932440  
; GENERAL INFORMATION:  
; APPLICANT: CHATTERJEE, DEB K.  
; APPLICANT: SHANDILYA, HARINI  
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,731  
; CLASSIFICATION: 435  
; FILING DATE: (Herewith)  
; APPLICATION NUMBER: 08/795,395  
; PRIORITY APPLICATION DATA:  
; FILING DATE: 04-FEB-1997  
; PRIORITY APPLICATION NUMBER: 08/794,546  
; FILING DATE: 03-FEB-1997  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/024,057  
; FILING DATE: 16-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ESMOND, ROBERT W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 0942.3440003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1374 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1368  
; US-08-910-731-3

Query Match 4.4%; Score 175.8; DB 2; Length 1374;  
Best Local Similarity 47.2%; Pred. No. 1.7e-41;  
Matches 568; Conservative 0; Mismatches 632; Indels 3; Gaps 1;

QY 2000 GGATCGGGGATTAAGACCTCATTTAGAGACAGTGGGAGATTCTGCTTCATGCTTGGA 2059  
DB 86 GGCTGGATGACGTGGGCTCCTCACTGAAGTGGGTCGGAAGACATCAAGTCAAGATCCAG 145  
QY 2060 CCCACCCACACCTGCGGACGCTGAGACCTGGGACGACGATCCTGACAGAGCGGGCCATGA 2119  
DB 146 CCACCCCTGCTGACAGAGCTCAAGCTTACGACCAATGATGCTGCTGCTGCTGCTG 205  
QY 2120 AGACCTGTGTGTCGAAGCTGAGGACATCCACCTGCAAGATACAGACCTGATGTTAGAA 2179  
DB 206 GTCTGTGTCTCCAGAGGCTGCAAGATCCCACTTGTATGATCCAGAGCTGAGCTTGACA 265  
QY 2180 ATGCAAGATTACCC---CTGTGTGTGACAGACCTCTGAGAAATGCTCATGAGCCAAACGTA 2236  
DB 266 ACTGACGCTTACGAGAACTGCTGTGGGTCTGCTCATATGCTGCTGCTGCTGCTGCTGCTA 325

QY 2237 ACCTAAGATCCCTCAACTTGGAGGACCCACCTGAAGAGAGATGTAAAGATGGCGT 2296  
DB 326 CCTGTGTGAATTAATCATCTCAATGACCAACCTCTGGGGGATGAAGGCTGAAAGCTGCTCT 385  
QY 2297 GTGAAGCCTTAATAACCCCAAAATGTTTGTGAGTCTTTGAGGCTGATTTGCTGTGAT 2356  
DB 386 GTGAAGGATCCGGGAGCCCCCAGTCCCGCTTGTGAAGAGCTTCAAGTTGAATTAATGTAAC 445  
QY 2357 TGACCAATGCTGTTTACCTGAAGATCTCCCAATGCTTACGACCTTCCCGAGCTGAAT 2416  
DB 446 TGACAGCTACAGCTGCGAGCCCTGCGCTTCACTGTCTCAGGGTGAACCTTGACTTTAAG 505  
QY 2417 CTCTGAGCTGCGACAGAAACAGGTGACAGACAGAGATTAATGCTCTCACTGATGCTCT 2476  
DB 506 AGCTAGTATTTAGCAACAATGATCTTCATGAGGCTGTATCAACATCTGTGTCCAGGGCC 565  
QY 2477 TGAAGTCTCCAGTGGCCCTGCGAGAACTGATATCTGAGGACCTGTGACATCAAGCCA 2536  
DB 566 TGAAGGATTTCTGCTGTCAACTGAGTCACTCAACTGGAGAACTGTGGTATCAATCAG 625  
QY 2537 CGGCTTGCAGAGTCTGCGCTCAAGCCCTGTGAGAACCGGAGCTTGAACACCTGTGCTC 2596  
DB 626 CCAACTGCAAGGATCTGTGTGATGTTGTGGCTTCAAAAGCTCACTGCAAGACTGAGT 685  
QY 2597 TATCCAAACAAGCCTGGGGAACGAAGGTGAATCTATGCTGTGATTCATGAGGCTTTC 2656  
DB 686 TGGGACGACAAAGCTGGGCAACAGAGCATTTGACAGACTGTGTCTCAGGACTGTGCTTC 745  
QY 2657 CCCACTGTATGTGACAGAGCTGATGATCACTGATCCACTGACACAGCTGCTGTG 2716  
DB 746 CCAGCTGACAGCTGAGACTGTGGCTTGGGACTGTGATGATCACTGACAGAGGCTGCA 805  
QY 2717 GTTTTCTTGCACTTGTGCTTAAGGTAATCAATGCTGACGACCTGAGGCTTACATTA 2776  
DB 806 AGGACCTGTGCTGTCTTCAAGAGCCAGACAGAGCTTGAAGACTCAGCTTACCTGCA 865  
QY 2777 ACCCTGTGAAGACATGAGCGCTGAAGCTTCTGTGCGAGGTCATGAGAGAACATCTTGT 2836  
DB 866 ATGAGCTGAAGATGAGGGTGCCTCACTGTGTGAGAGCTTGTAGAGCTTGTGCTGTC 925  
QY 2837 ATCTCAGAGCCTGAGATTGTGAAGTGTATCTGACCGCGCTGTGTGAGAGTCTGT 2896  
DB 926 AGCTGAGTCACTGTGGGTAAAGACCTGTAGCTCAGCTGCTCTTGTCCCACTTCT 985  
QY 2897 CTTGTGTATCTGAGAGACAGACACTGAGAGCTGTGATTCACGACATATGCCCTG 2956  
DB 986 GCTCGGTGTGACCAAAAACAGTTCTCTGTTGAGTTGCAATGACAGCAACCGCTG 1045  
QY 2957 GTGACGCTGGGCTGTGCTGCTGCTGCGGAGGACCTGAAGCAAAAAGAGTTTTCAGCA 3016  
DB 1046 GAGACTTCGGAGTCTGTGAGCTTTCAGAGGCTTGGGCTATCCGACACAGTGTGCTG 1105  
QY 3017 GACTCGGCTGAAGCAGATGTGACATGACTTGTGATGTGCTGTGAGGACATCTCTTGGCC 3076  
DB 1106 TGCTTTGTGTGGAACATGTATATGACAGACAGTGGCTGACAGCCTGTGCACTGTGTC 1165  
QY 3077 TTTCTGCAACCGGACATCTGACCACTTAACTGTGTGAGTGAATTAATTTCAATGCCAAG 3136  
DB 1166 TGCTGGCAACCGGACCTTGAAGGAACTGACCTCAGTAAACAATGAGTGGGGGACAG 1225  
QY 3137 GAATGATGAAGTGTGTGTGCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3196  
DB 1226 GTGTCTTCAACTGTGAGAGCTTCAAAACAGCCAGCTGATCTTTCAGACCTTGTTC 1285  
QY 3197 TGT 3199  
DB 1286 TGT 1288

RESULT 11  
US-08-795-395-3  
; Sequence 3, Application US/08795395



Patent No. 5965399  
GENERAL INFORMATION:  
APPLICANT: CHATTERJEE, DEB K.  
APPLICANT: SHANDILYA, HARINI  
TITLE OF INVENTION: Cloning and Expression of Rat Liver and  
NUMBER OF INVENTION: Porcine Liver Ribonuclease Inhibitor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVE., N.W., SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,395  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/024,057  
FILING DATE: 16-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ESMOND, ROBERT W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0942.3440002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1374 base pairs  
TYPE: nucleic acid  
STRADEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1368  
US-08-795-395-3

Query Match 4.4%; Score 175.8; DB 2; Length 1374;  
Best Local Similarity 47.2%; Pred. No. 1.7e-41;  
Matches 568; Conservative 0; Mismatches 632; Indels 3; Gaps 1;

QY 2000 GGATGCGGATTAAGACCTCTATGAGAGCAAGTGGAAATTCTGCTTCATGCTTGGCA 2059  
DB 86 GGCTGATGACTGTGGCTCACTGAAAGTGGGTCGCAAGATCAAGATCCAGG 145  
QY 2060 CCCACCCACACTGCGGAGCTGAGACTGCGGAGAGACATCTCTGACAGAGCGGCGCATGA 2119  
DB 146 CCAACCTGCGCTGACAGAGCTCAAGCTCAAGCAACCAAGAACTGGGTATGCTGTGG 205  
QY 2120 AGACCTGTGTGCCAAGCTGAGGACATCCACCTGCAAGATACAGACCTGATGTTTAA 2179  
DB 206 GTCTGTCTCCAGGCGCTTGCAGAAATCCACTTGTAAATCCAGAACTGAGCTTCGA 265  
QY 2180 ATGCAAGATTATCC--CTGGTGTGAGACCTCTGAGATCTGTACATGCGCAACCGTA 2236  
DB 266 ACTGACGCTTACGAGAGCTGGCTGTGGGTCCTCTCGATGATGCTGGGCTTTTGTCTA 325  
QY 2237 ACCTTAAGTCCCTCAACTTGGAGGACACCTCACTGAAGAGAGATGAAGATGGCGT 2296  
DB 326 CCGTCCGTAATCAATCAATGACCAACCTCTGCGGAGATGAAGCGCTGAAGCTGCTCT 385  
QY 2297 GTGAAGCTTTAAACACCAAAATGTTTGTGAGATCTTTTGAAGCTGATGCTGTGAT 2356  
DB 386 GTGAAGACTCCGGAGACCCCAAGTCCGTCTTGAAGACTTCAAGTTGAATATCTGAAC 445

QY 2357 TGACCATGCTGTTTACTGTGAAGATCTCCAAATCTTACAGACTCCCCAGCCTGAAT 2416  
DB 446 TCACAGTACCAAGCTGCGAGCCCTGCGCTCAGGCTCAGGATGAACCTGACTTTAAAG 505  
QY 2417 CTGAGAGCTGAGAAACAAAGGAGACAGACGAGGAGTAATGCTCTGATGAGCT 2476  
DB 506 AGCTAATTTAGCAACAATATATCTTCAATAGGCTGTATCAACATCTGTGCCAGGCC 565  
QY 2477 TGAAGTCTCCAGTGCCTCCGACAGAGCTGATATCTGAGAGATGTGGCATCAAGCCA 2536  
DB 566 TGAAGATTTGCTGCTCACTGAGATCACTCAATGAGAACTGTGTATCAATCAG 625  
QY 2537 CCGGTGCAAGATCTGCGCTCAAGCCCTGTCAAGCAACCGAAGCTTGAACAACCTGTGCC 2596  
DB 626 CCAACTGCAAGATCTGTGTATGTGTGCGCTCAAGACCTCACTGCAACAACTGAGACT 685  
QY 2597 TATCCAAACAGCCTGGGAGAACAGAGGTGAATTAATCTAGTGTGATCCATGAGGCTTC 2656  
DB 686 TGGGACGACAAAGCTGGGCAACAGGCAATTGACGACTGTGCTCAGGACTGCTCTTC 745  
QY 2657 CCACTGTATCTGCAAGGCTGATGCTGAATCAGTGCACCTGAGACAGCTGCTGTG 2716  
DB 746 CCAAGTCAAGCTGAGACTGTGAGCTGTGGGCTGTGGAGCTGTGATGATCACTGCAAGAGGCTGCA 805  
QY 2717 GTTTCTTCACTTGCCTTAAGGTAACTCATGAGCTGACGCACTGAGCCTTACATGA 2776  
DB 806 AGGACCTGTGCTGTGCTTCAAGACCAAGACAGACCTGAAAGAACTCAGCTTACCTGCA 865  
QY 2777 ACCCTGAGAGAGAAAGAGGCTGAAAGCTTGTGAGAGGTATGAGAGAACTTGTGTC 2836  
DB 866 ATGAGCTGAAGAGAGGAGTCCCACTGCTGTGTGAGAGCTGTGAGAGCTGCTGCTGTC 925  
QY 2837 ATCTCAGGACCTGAGTGTGTAAGTGTATCTTCACTCAGCGCGCTGTGTGAGAGTCTGT 2896  
DB 926 AGCTGAGTCACTGTGGTAAAGACTGTATCTCAAGCTGAGCTGCTTGTCCCACTTCT 985  
QY 2897 CTTGTGTATCTCAAGAGACGACACTGTAAAGCTGAGATCTCAAGCAATGCGCTG 2956  
DB 986 GCTGTGTGTGACCAAAACAGTCTCTGTGTGATGCAATGACAGCAACCGCTGG 1045  
QY 2957 GTGACGGTGGGTTGCTGCGCTGTGCGAGGACGAAAGCAAAAGACGTTTGTGACGA 3016  
DB 1046 GAGACTCGGAGGTGTGAGCTTTTGCAGAGCCCTGCGCTATCCGACCAAGTGTGCTG 1105  
QY 3017 GACTCGGTTGAGAGCAATGTGACTGACTTCTGATGCTGTGAGAGCACTCTCTTGGGCC 3076  
DB 1106 TGTCTTGTGCTGAGAGCTGTATGTGACAGCAAGTGTGACAGAGCTTGTGCACTGTCC 1165  
QY 3077 TTTCTGCAACCGGCACTGACAGCTTAACTGTGTGAGATTAATCTTCACTGCTCAAAG 3136  
DB 1166 TGTGTGCAACCGGCACTGTGAGGAACTGAGACTCAAGTAACTGCAATGAGGAGCAACG 1225  
QY 3137 GAATGATGAACGTGTGCTGCTTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 3196  
DB 1226 GTGTCTTCAACTCTGTGAGAGCTTCAAAACAGCCAGCTGATCTTCAAGAGCTGTGCC 1285  
QY 3197 TGT 3199  
DB 1286 TGT 1288

RESULT 12  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHRIFFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner

```
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZpt-F18
US-08-232-463-14

Query Match
Best Local Similarity 1.5%; Score 61; DB 1; Length 7218;
Matches 4; Conservative 225; Mismatches 130; Indels 0; Gaps 0;

QY 264 GAGAGAGCAGCGATGACATGAAATTTCAACAGCTATGAAACAGAGGTGCAC 323
DB 1421 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1362
QY 324 AGCAGCAGACAGAGACAGAAATTTCAACAGCTATGAAACAGAGGTGCACAGC 383
DB 1361 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1302
QY 384 AGCAGACAGAGAAACAGAGCATGTGAGGTGACATGGAGCTACAGAGTCACTGAT 443
DB 1301 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1242
QY 444 GACCAATTCCTGAGAGAGAGATGATGCTGTTTGAATAACACTGCTGCTAGCTG 503
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QY 504 GCCGAAATGCAACGTTGCTGCTGTTGATTGACAGCGGTGGGGCTTCGGCTCTG 563
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## RESULT 13

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US-09-023-655-395
; Sequence 395; Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
; APPLICANT: Susan G. Stuart
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 395:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPLPLB02
CLONE: 153338
US-09-023-655-395

Query Match
Best Local Similarity 1.5%; Score 60; DB 4; Length 376;
Matches 134; Conservative 0; Mismatches 106; Indels 1; Gaps 1;

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QY 3034 TGTGACACTCTTCGATGTGCTGTGAGGCACTCTCTTGCGCCCTTCTCGAACCGGAT 3093
DB 155 TGTGCTCATACATAGATGTGTGAGATTTTTCATGATTCAGTATGAGACACAGCATTC 214
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US-09-949-016-16600
; Sequence 16600; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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OM nucleic - nucleic search, using SW model

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Perfect score: 4035

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Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 287871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	4035	100.0	4035	US-10-066-521-5	Sequence 5, Appli
3	3166.2	78.5	3885	US-10-860-761-3	Sequence 3, Appli
4	3166.2	78.5	3900	US-10-399-443-23	Sequence 23, Appli
5	3166.2	78.5	3900	US-10-677-943-23	Sequence 23, Appli
6	3133.9	77.8	3830	US-10-216-645-3	Sequence 3, Appli
7	3133.6	77.7	3489	US-10-416-642-3	Sequence 3, Appli
8	3133.6	77.7	3926	US-10-216-645-1	Sequence 1, Appli
9	2900.6	71.9	3226	US-10-092-900A-347	Sequence 347, App
10	1278	31.7	3447	US-10-399-443-5	Sequence 5, Appli
11	1278	31.7	3447	US-10-677-943-5	Sequence 5, Appli

12	1152.8	28.6	1157	17	US-10-399-443-1	Sequence 1, Appli
13	1152.8	28.6	1157	17 <th>US-10-677-943-1</th> <th>Sequence 1, Appli</th>	US-10-677-943-1	Sequence 1, Appli
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26	419.2	10.4	2575	9 <th>US-09-848-035-7</th> <th>Sequence 7, Appli</th>	US-09-848-035-7	Sequence 7, Appli
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28	419.2	10.4	2883	17 <th>US-10-161-493-3</th> <th>Sequence 3, Appli</th>	US-10-161-493-3	Sequence 3, Appli
29	419.2	10.4	3172	18 <th>US-10-398-037-74</th> <th>Sequence 74, Appli</th>	US-10-398-037-74	Sequence 74, Appli
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45	357.6	8.9	3466	17 <th>US-10-108-260A-718</th> <th>Sequence 718, App</th>	US-10-108-260A-718	Sequence 718, App

#### ALIGNMENTS

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; Sequence 5, Application US/10124498  
; Publication No. US20030017983A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Wang, Weiye  
; APPLICANT: Blatcher, Maria  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-367001  
; CURRENT APPLICATION NUMBER: US/10/124,498  
; CURRENT FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 10/066,521  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/318,645  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/265,231  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 4035  
; TYPE: DNA  
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; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(4032)  
US-10-124-498-5  
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Best Local Similarity 100.0%; Pred. No. 0;  
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Qy 2941 ACGGACATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000  
Db 2941 ACGGACATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000  
Qy 3001 AACAGTGTCTGACGAGACTCGGCTTGAAGGATGTGACCTTCTGATGTCTGTG 3060  
Db 3001 AACAGTGTCTGACGAGACTCGGCTTGAAGGATGTGACCTTCTGATGTCTGTG 3060  
Qy 3061 GCACTCTCTTGGCCCTTCTCTGCAACCGGACTGACAGCTTAACCTGGTGCAGAT 3120  
Db 3061 GCACTCTCTTGGCCCTTCTCTGCAACCGGACTGACAGCTTAACCTGGTGCAGAT 3120  
Qy 3121 AACCTTCAGTCCCAAGAAATGATGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3180  
Db 3121 AACCTTCAGTCCCAAGAAATGATGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3180  
Qy 3181 TTACGATTAATTTGGCTGTGAAATGAGCATCCCTGTGCAAAATAGAGAGCTGTG 3240  
Db 3181 TTACGATTAATTTGGCTGTGAAATGAGCATCCCTGTGCAAAATAGAGAGCTGTG 3240  
Qy 3241 GAAAGTCACTACTCAAGCCCGAGTCTGTAAATGACGATGATGTGCACTTCTTTG 3300  
Db 3241 GAAAGTCACTACTCAAGCCCGAGTCTGTAAATGACGATGATGTGCACTTCTTTG 3300

Qy 3301 GATGACCGACAAATATGAGACTTCTTCCGGCTCCCTGAAGCCGGGATGCGCAT 3360  
Db 3301 GATGACCGACAAATATGAGACTTCTTCCGGCTCCCTGAAGCCGGGATGCGCAT 3360  
Qy 3361 GCTTGTGTGGGATGAAACCCAGAGAAAGAGCTGTGTGTGTGTGTGTGTGTGT 3420  
Db 3361 GCTTGTGTGGGATGAAACCCAGAGAAAGAGCTGTGTGTGTGTGTGTGTGTGT 3420  
Qy 3421 TTCAAGACATGACCAATTTGCCAATGCTCTGTGCTGTGCTGTGCTGTGCTGTG 3480  
Db 3421 TTCAAGACATGACCAATTTGCCAATGCTCTGTGCTGTGCTGTGCTGTGCTGTG 3480  
Qy 3481 CAGAGATTGACCAAGTGAAGAGCTCCCGCAACCAATGAGCAGACCGAACA 3540  
Db 3481 CAGAGATTGACCAAGTGAAGAGCTCCCGCAACCAATGAGCAGACCGAACA 3540  
Qy 3541 CAGATTAATTTGATGATGATTAATCCGAGCTGTGTGTAATCTGTGAGCTGAA 3600  
Db 3541 CAGATTAATTTGATGATGATTAATCCGAGCTGTGTGTAATCTGTGAGCTGAA 3600  
Qy 3601 GGGCTTGTGATCCAAAGTGTGATGATGACCAAGGATTAAGCTGTGCTGTGAG 3660  
Db 3601 GGGCTTGTGATCCAAAGTGTGATGATGACCAAGGATTAAGCTGTGCTGTGAG 3660  
Qy 3661 GAGCTGAGCTGAGGGGCTGTGTGTCAAAGTGTGATGACCAAGGATTAAGCT 3720  
Db 3661 GAGCTGAGCTGAGGGGCTGTGTGTCAAAGTGTGATGACCAAGGATTAAGCT 3720  
Qy 3721 CACTGGAGCGGCTGTGGCTTAAGGGCTGTGTGTTAAAGTGTGATGACCAAGCG 3780  
Db 3721 CACTGGAGCGGCTGTGGCTTAAGGGCTGTGTGTTAAAGTGTGATGACCAAGCG 3780  
Qy 3781 GTGTCTGTGATCACTGGAGCGGCTGTGGCTTAAGGGCTGTGTGTTAAAGTGT 3840  
Db 3781 GTGTCTGTGATCACTGGAGCGGCTGTGGCTTAAGGGCTGTGTGTTAAAGTGT 3840  
Qy 3841 CACAGCGGTGTGGCTGTGTGTCAGTGGAGCGGCTGTGGCTGTGTGTCAAAGT 3900  
Db 3841 CACAGCGGTGTGGCTGTGTGTCAGTGGAGCGGCTGTGGCTGTGTGTCAAAGT 3900  
Qy 3901 GCTGATGACCAAGCGGTGTGTGTCAGTGGAGCGGCTGTGGCTGTGTGTCAG 3960  
Db 3901 GCTGATGACCAAGCGGTGTGTGTCAGTGGAGCGGCTGTGGCTGTGTGTCAG 3960  
Qy 3961 TCCAAGTGTGATGACCAAGCGGTGTGTGTCAGTGGAGCGGCTGTGGCTG 4020  
Db 3961 TCCAAGTGTGATGACCAAGCGGTGTGTGTCAGTGGAGCGGCTGTGGCTG 4020  
Qy 4021 GGGCTGTGTGCTTAA 4035  
Db 4021 GGGCTGTGTGCTTAA 4035

RESULT 2  
US-10-066-521-5  
; Sequence 5, Application US/1006521  
; Publication No. US20030027757A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Wang, Weiye  
; APPLICANT: Blatcher, Maria  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
; FILE REFERENCE: 07334-334001  
; CURRENT FILING DATE: 2002-06-25  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/265, 231  
; PRIOR FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5  
LENGTH: 4035  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(4032)  
US-10-066-521-5

Query Match 100.0%; Score 4035; DB 14; Length 4035;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAGCAAAATCGCTCACTTTTCAGCTACGGGCTGCAATGGTGTCTATAG 60  
DB 1 ATGAGAGAGCAAAATCGCTCACTTTTCAGCTACGGGCTGCAATGGTGTCTATAG 60  
QY 61 CTAGCAAGAGAAATTTCAAGCATTCAGAAATTAATTAAGAAATTTCAAGATCG 120  
DB 61 CTAGCAAGAGAAATTTCAAGCATTCAGAAATTAATTAAGAAATTTCAAGATCG 120  
QY 121 ACCACATGCTCTATTCACAGATTGAAATCGAATGCAACGTGAAATGCTGCACTC 180  
DB 121 ACCACATGCTCTATTCACAGATTGAAATCGAATGCAACGTGAAATGCTGCACTC 180  
QY 181 CTCTTGCAATGATATTATGAGCATGCTGGCTGGCTGAGCTGATGATGCAATCTTTGAA 240  
DB 181 CTCTTGCAATGATATTATGAGCATGCTGGCTGGCTGAGCTGATGATGCAATCTTTGAA 240  
QY 241 AACATGAACCTGCGAACCCTCTCGGAGAAAGCAAGGAGATGACATGAAAAAATTTCAAA 300  
DB 241 AACATGAACCTGCGAACCCTCTCGGAGAAAGCAAGGAGATGACATGAAAAAATTTCAAA 300  
QY 301 GCTATGAAACAAGAGGTGCAACAGCAGACAGACAGAAACAAGAAATTTCAACAAGCT 360  
DB 301 GCTATGAAACAAGAGGTGCAACAGCAGACAGACAGAAACAAGAAATTTCAACAAGCT 360  
QY 361 ATGGAACAAGAGGTGCAACAGCAGACAGACAGAAACAAGAAATTTCAAGAGTGAACA 420  
DB 361 ATGGAACAAGAGGTGCAACAGCAGACAGACAGAAACAAGAAATTTCAAGAGTGAACA 420  
QY 421 TGGGACTCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGAGAGATGACGTGTAGT 480  
DB 421 TGGGACTCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGAGAGATGACGTGTAGT 480  
QY 481 TTTGAAAAACATGCTGCTGACCTGCGGAAATGCAAGCTGGCTGTGCTTTGATTC 540  
DB 481 TTTGAAAAACATGCTGCTGACCTGCGGAAATGCAAGCTGGCTGTGCTTTGATTC 540  
QY 541 GACCGGTGGGCTTCGCGCTGCAAGGTGTTCTGCAAGAAATGCAAGAAATTTGGAAA 600  
DB 541 GACCGGTGGGCTTCGCGCTGCAAGGTGTTCTGCAAGAAATGCAAGAAATTTGGAAA 600  
QY 601 TCGGCTCAAGCAGAGATGCTGCTGCTGGGCGCAAGGAGCTTACCAAGGAAATG 660  
DB 601 TCGGCTCAAGCAGAGATGCTGCTGCTGGGCGCAAGGAGCTTACCAAGGAAATG 660  
QY 661 TTCTCTCAAGTCTTCTCTCCCGTTAGAGATGACAGCGGAAAGAGAGAGAGAGCTGTC 720  
DB 661 TTCTCTCAAGTCTTCTCTCCCGTTAGAGATGACAGCGGAAAGAGAGAGAGAGCTGTC 720  
QY 721 ACAGAGTTCATCTCAGAGAGTGGCAGACTCCAGGCTCCGATGACGAGATCATATGCC 780  
DB 721 ACAGAGTTCATCTCAGAGAGTGGCAGACTCCAGGCTCCGATGACGAGATCATATGCC 780  
QY 781 CGACCAAGAAAGGCTGTGTTCAATGACGTTTCAGATGACCTGGGCTCTGCTCAAC 840  
DB 781 CGACCAAGAAAGGCTGTGTTCAATGACGTTTCAGATGACCTGGGCTCTGCTCAAC 840  
QY 841 AATGACAAAGAGCTGCAAGAGCTGGGCTGAGAGAGAGCTCGTTCAACCTCAAGC 900  
DB 841 AATGACAAAGAGCTGCAAGAGCTGGGCTGAGAGAGAGCTCGTTCAACCTCAAGC 900

QY 901 AGTCTGTGAGAGAGGTCTCTCCCTGAGGCTTCTGATCCGACACCGTCAGAGAGCTG 960  
DB 901 AGTCTGTGAGAGAGGTCTCTCCCTGAGGCTTCTGATCCGACACCGTCAGAGAGCTG 960  
QY 961 GGCACAGAGAGAGCTCAAGTCAAGAGTGTGCTCCCGTTACCTGTTAGTTAGAGATC 1020  
DB 961 GGCACAGAGAGAGCTCAAGTCAAGAGTGTGCTCCCGTTACCTGTTAGTTAGAGATC 1020  
QY 1021 TCCGGGAAACAAGATCCACTTGTCTCTTGAAGCGCGGATTTGGTAGCATCAGAAC 1080  
DB 1021 TCCGGGAAACAAGATCCACTTGTCTCTTGAAGCGCGGATTTGGTAGCATCAGAAC 1080  
QY 1081 CAAGGTTGCGTGGATCAGAAACAACCGTGAAGTGTCCACGACGAGTCCAGGTCCGCC 1140  
DB 1081 CAAGGTTGCGTGGATCAGAAACAACCGTGAAGTGTCCACGACGAGTCCAGGTCCGCC 1140  
QY 1141 GTGGGCTCTCATCTGCGTGGCCCTGCAAGTCAAGACGAGTGGGAGAGAGCTGCGC 1200  
DB 1141 GTGGGCTCTCATCTGCGTGGCCCTGCAAGTCAAGACGAGTGGGAGAGAGCTGCGC 1200  
QY 1201 CCTTCAACCAAGCTCAAGGCTGCAAGGCTGCAAGGCTTTGTGTTCAATCAGCTCACCCCT 1260  
DB 1201 CCTTCAACCAAGCTCAAGGCTGCAAGGCTGCAAGGCTTTGTGTTCAATCAGCTCACCCCT 1260  
QY 1261 CGAGGCTGTGCTCGGCTGCTCAATCTGAGAGAAAGATGTCGGAAGCGCTTCTGC 1320  
DB 1261 CGAGGCTGTGCTCGGCTGCTCAATCTGAGAGAAAGATGTCGGAAGCGCTTCTGC 1320  
QY 1321 CGATGCTGTGAGAGAGTGTGAATGAGAGTCAAGTGTGTTGATGATGAGAGAGCTCATG 1380  
DB 1321 CGATGCTGTGAGAGAGTGTGAATGAGAGTCAAGTGTGTTGATGATGAGAGAGCTCATG 1380  
QY 1381 GTTCAAGAGCTCGGAGAGTCTGAGCTCGTCTGTTTCATATGAACATCTTCTCCA 1440  
DB 1381 GTTCAAGAGCTCGGAGAGTCTGAGCTCGTCTGTTTCATATGAACATCTTCTCCA 1440  
QY 1441 GACAGCCACTGTGAGAGTACTAACACTTCTTCCACCTCACTCTCCAGAGCTTGTGCC 1500  
DB 1441 GACAGCCACTGTGAGAGTACTAACACTTCTTCCACCTCACTCTCCAGAGCTTGTGCC 1500  
QY 1501 GCTTTGATCAAGTGTGAGAGGCTGGAATTCAGAGCAAGCTCTGCTCCCTGTACGTT 1560  
DB 1501 GCTTTGATCAAGTGTGAGAGGCTGGAATTCAGAGCAAGCTCTGCTCCCTGTACGTT 1560  
QY 1561 GAGAAGCAAAAGAGTCCATGAGCTTAAACAGGCAAGCTTCAATATCACTGCTTTGG 1620  
DB 1561 GAGAAGCAAAAGAGTCCATGAGCTTAAACAGGCAAGCTTCAATATCACTGCTTTGG 1620  
QY 1621 ATGAAGGCTTCTGTTTGGCTCTGAGCGAACAAGTGAAGAGCCACTGGAAGTCTG 1680  
DB 1621 ATGAAGGCTTCTGTTTGGCTCTGAGCGAACAAGTGAAGAGCCACTGGAAGTCTG 1680  
QY 1681 CTGGGCTGTCCGTTCCCTGGGAGTGAAGAGAGCTTCTGCACTGGGCTCTCTGTTG 1740  
DB 1681 CTGGGCTGTCCGTTCCCTGGGAGTGAAGAGAGCTTCTGCACTGGGCTCTCTGTTG 1740  
QY 1741 GGTCAAGAGCTTAATGCAACCAAGAGAGACCTTGAAGAGAGCTTCACTGTCTTTTC 1800  
DB 1741 GGTCAAGAGCTTAATGCAACCAAGAGAGACCTTGAAGAGAGCTTCACTGTCTTTTC 1800  
QY 1801 GAGACTCAAGCAAAAGATTTGCTGCTGAGCAATTAACAGCTTCAAGAGATGCTGCTT 1860  
DB 1801 GAGACTCAAGCAAAAGATTTGCTGCTGAGCAATTAACAGCTTCAAGAGATGCTGCTT 1860  
QY 1861 CGGATTAACCAAGAGCTGGAATTAATGAGATCTTCTGCTGCTGCAAGAGATGCTGCT 1920  
DB 1861 CGGATTAACCAAGAGCTGGAATTAATGAGATCTTCTGCTGCTGCAAGAGATGCTGCT 1920  
QY 1921 TTGCGGAAATTTCCGGTGAATGTCAAGAGAGATCTTCCAGAGATGAGTCCGCTGAGCA 1980  
DB 1921 TTGCGGAAATTTCCGGTGAATGTCAAGAGAGATCTTCCAGAGATGAGTCCGCTGAGCA 1980  
QY 1981 TGTCTGTGTCTCTCTATGAGTCCGGATTAAGACCTCATTTGAGAGAGAGTGGAAAT 2040



Db 1981 TGTCTGTGTCCTCTCTATGATGCGGGATAGACCTCATATGAGAGAGAGGGAAGAT 2040  
Qy 2041 TTTCGCTCATGCTTGGACCCACACCGTGGGAGCTGGACCTGGGGAGAGCATC 2100  
Db 2041 TTTCGCTCATGCTTGGACCCACACCGTGGGAGCTGGACCTGGGGAGAGCATC 2100  
Qy 2101 CTGACAGAGCGGGCCATGAGAGCCCTGTGTGCAAGCTGAGGCACTCCACCTGCAAGTA 2160  
Db 2101 CTGACAGAGCGGGCCATGAGAGCCCTGTGTGCAAGCTGAGGCACTCCACCTGCAAGTA 2160  
Qy 2161 CAGACCTGATGTTTGAAGATCAAGATTACCCCTGTGTGCAAGCTTGTGAAGATC 2220  
Db 2161 CAGACCTGATGTTTGAAGATCAAGATTACCCCTGTGTGCAAGCTTGTGAAGATC 2220  
Qy 2221 GTCATGCGCAACCGGATCTAAGATCCCTCAACTTGGAGGCAACCACTGAAAGGAAG 2280  
Db 2221 GTCATGCGCAACCGGATCTAAGATCCCTCAACTTGGAGGCAACCACTGAAAGGAAG 2280  
Qy 2281 GATGTAAAGATGCGCTGTGAAGCTTAAACACCCAAATGTTTGTGAAGCTTTGAGG 2340  
Db 2281 GATGTAAAGATGCGCTGTGAAGCTTAAACACCCAAATGTTTGTGAAGCTTTGAGG 2340  
Qy 2341 CTGATGCTGTGATGATGACCCATGCTGTTAAGATCTCCAAATCTTACGACC 2400  
Db 2341 CTGATGCTGTGATGATGACCCATGCTGTTAAGATCTCCAAATCTTACGACC 2400  
Qy 2401 TCCCCAGCTGTAATCTCTGAGCTGGCAGAAACAGGTGACAGACAGGAGTAATG 2460  
Db 2401 TCCCCAGCTGTAATCTCTGAGCTGGCAGAAACAGGTGACAGACAGGAGTAATG 2460  
Qy 2461 CCTCTAGTGAAGCTTGAAGATCTCCAGTGGCCCTGACAGAGCTGATCTGAGAGC 2520  
Db 2461 CCTCTAGTGAAGCTTGAAGATCTCCAGTGGCCCTGACAGAGCTGATCTGAGAGC 2520  
Qy 2521 TGTGGCATCAGACCGAGTTGCCAGAGTCTGAGCTCAAGCCCTGTGACAGACCGAGC 2580  
Db 2521 TGTGGCATCAGACCGAGTTGCCAGAGTCTGAGCTCAAGCCCTGTGACAGACCGAGC 2580  
Qy 2581 TTGACACACTGTGCTTATCCAAACAGCTGGGGAACAGAGGTGTAATCTACTGTGT 2640  
Db 2581 TTGACACACTGTGCTTATCCAAACAGCTGGGGAACAGAGGTGTAATCTACTGTGT 2640  
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Db 2641 CGATCATGAGGCTTCCCACTGATCTGAGAGGCTGATGCTGAATCAAGTGCACCTG 2700  
Qy 2701 GACACGCTGCTGTGTTTCTTTCACCTTGTGCTTATGCTGATCTGATGCTGACGAC 2760  
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Qy 2761 CTGAGCTTACATGACCTGTGAGAGCAATGCGTGAAGCTTCTGTGCAAGGTCATG 2820  
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Db 2881 TGTGTGAGAGTCTGCTGTGTGATCTGAGAGACAGACCTGAAGAGCTGTGATCTC 2940  
Qy 2941 ACGGACATGCTGCTGTGTGAGAGGCTGTGCTGTGTGAGAGGACCTGAAGCAAAAG 3000  
Db 2941 ACGGACATGCTGCTGTGTGAGAGGCTGTGCTGTGTGAGAGGACCTGAAGCAAAAG 3000  
Qy 3001 AACGATGTTTGAAGAGCTGGGTTGAAGGATGATGATCTTCTGATGCTGTGAG 3060  
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Qy 3061 GCACTCTCTTGGCCCTTCTGCAACCGGACCTGACCAAGTCTAAACCTGGTGCAGAT 3120  
Db 3061 GCACTCTCTTGGCCCTTCTGCAACCGGACCTGACCAAGTCTAAACCTGGTGCAGAT 3120

Db 3061 GCACTCTCTTGGCCCTTCTGCAACCGGACCTGACCAAGTCTAAACCTGGTGCAGAT 3120  
Qy 3121 AACTCAGTCCAAAGATGATGAGCTGTGTGGCTTGTGCTTGTCCAGTCTAAC 3180  
Db 3121 AACTCAGTCCAAAGATGATGAGCTGTGTGGCTTGTGCTTGTCCAGTCTAAC 3180  
Qy 3181 TTACGATTAATGCTGTGAAATGAGATCCCTGTGCAATTAAGAGCTGTGAG 3240  
Db 3181 TTACGATTAATGCTGTGAAATGAGATCCCTGTGCAATTAAGAGCTGTGAG 3240  
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Qy 3301 GATGACGACCAAAATGAGCTTACTTCCGCTCCCTGAAAGCGGAGCATGCTGAT 3360  
Db 3301 GATGACGACCAAAATGAGCTTACTTCCGCTCCCTGAAAGCGGAGCATGCTGAT 3360  
Qy 3361 GCTTGTGTGGGAGTGAACCCAGAGCAAGAGAGCTGTGTGCTTGTGCTGAGAGC 3420  
Db 3361 GCTTGTGTGGGAGTGAACCCAGAGCAAGAGAGCTGTGTGCTTGTGCTGAGAGC 3420  
Qy 3421 TTCAAGAGCTGACAGATTTGCAAGTCTGTCTGTGCAAGCGCAATGTGATCTC 3480  
Db 3421 TTCAAGAGCTGACAGATTTGCAAGTCTGTCTGTGCAAGCGCAATGTGATCTC 3480  
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Db 3661 GAGCTGAGCTGAGGAGCTGTGTGTCACAGTGTGATGATGATGATGATGATGATG 3720  
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Db 3721 CACTGGAGCGGCTGTGCTTGAAGGCTGTGTCTTAAACAGTGTGATGATGATG 3780  
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Db 3781 GTGTCTGTGATGATGAGGCTGTGCTGAGGCTGTGTCTTCAACAGTGTGATGATG 3840  
Qy 3841 CACAGCGTGTGCTGTGATCTGAGAGGCTGTGAGGCTGTGTCTTCAACAGT 3900  
Db 3841 CACAGCGTGTGCTGTGATCTGAGAGGCTGTGAGGCTGTGTCTTCAACAGT 3900  
Qy 3901 GCTGATGACCAAGCGGCTGTGCTGATGATGATGATGATGATGATGATGATG 3960  
Db 3901 GCTGATGACCAAGCGGCTGTGCTGATGATGATGATGATGATGATGATGATG 3960  
Qy 3961 TCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4020  
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Qy 4021 GGGCTGTGTCTTAA 4035  
Db 4021 GGGCTGTGTCTTAA 4035

RESULT 3  
US-10-860-761-3  
; Sequence 3, Application US/10860761  
; Publication No. US2004024875A1  
; GENERAL INFORMATION:  
; APPLICANT: WYETH

TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS  
FILE REFERENCE: AM101318  
CURRENT APPLICATION NUMBER: US/10/860,761  
CURRENT FILING DATE: 2004-06-03  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 3885  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3603)  
US-10-860-761-3

Query Match 78.5%; Score 3166.2; DB 18; Length 3885;  
Best Local Similarity 96.2%; Pred. No. 0;  
Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;

1 ATGGAAGAGCAAAATCGCTCACTTTTTCAGCTACGGGCTGCAATGGTCTCTATGAG 60  
154 ATGGAAGAGCAAAATCGCTCACTTTTTCAGCTACGGGCTGCAATGGTCTCTATGAG 213  
61 CTAGCAAGAGAAATTTCAAGCATTTCAAGAAATTTCAAGAAATTTCAAGAAATCG 120  
214 CTAGCAAGAGAAATTTCAAGCATTTCAAGAAATTTCAAGAAATTTCAAGAAATCG 273  
121 ACCACATGCTCTATTCACAGATTGAAATCGAAATGCAAGTGAATGTCGCACTC 180  
274 ACCACATGCTCTATTCACAGATTGAAATCGAAATGCAAGTGAATGTCGCACTC 333  
181 CTCTTGATGATATTTATGAGCATGCTGCGCTGGGCTACGTCATTAGCATCTTTGAA 240  
334 CTCTTGATGATATTTATGAGCATGCTGCGCTGGGCTACGTCATTAGCATCTTTGAA 393  
241 AACATGAACCTGCGCAACCTCTCGGAGAAAGCAAGGATGACATGAAAA----- 289  
394 AACATGAACCTGCGCAACCTCTCGGAGAAAGCAAGGATGACATGAAAAAATTACCA 453  
290 ----- 289  
454 GAAGATCTGAAAGCAAGATGATGACCAAGAACCAAGCAAGAAAGATTCAGAAATT 513  
290 -----AAATTTCA 297  
514 TCACAACTGTGCAACAAATATGTCACAGCTGCAAGAACCAAGAAATTTCA 573  
298 CAAGTATGAAACAAGAGGTGCCACAGACAGACAGACAGAAACAAGAAATTTCA 357  
574 CAAGTATGAAACAAGAGGTGCCACAGACAGACAGACAGAAACAAGAAATTTCA 633  
358 GCTATGAAACAAGAGGTGCCACAGACAGACAGACAGAAACAAGACATGGAAGTAC 417  
634 GCTATGAAACAAGAGGTGCCACAGACAGACAGACAGAAACAAGACATGGAAGTAC 693  
418 ACATGGGACTCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGAGATGTAAGTCTG 477  
694 ACATGGGACTCAAGAGTCAAGTATGACAAATTCGCTGAGAGAGAGATGTAAGTCTG 753  
478 AGTTTGAACCACTGCTGCTGACCTGCGGAAATGCAAGCTTGGCTGCTTTGAT 537  
754 AGTTTGAACCACTGCTGCTGACCTGCGGAAATGCAAGCTTGGCTGCTTTGAT 813  
538 TCAGACGGGTGGGCTTCGCGCTGCAAGGATGCTGCAAGGAAATGCAAGAAATTTGAG 597  
814 TCAGACGGGTGGGCTTCGCGCTGCAAGGATGCTGCAAGGAAATGCAAGAAATTTGAG 873  
598 AAATCGGCTTACGCAAGAGATCGTGTGCTGCTGCGGCGCAAGGTGACTTACAGGGA 657  
874 AAATCGGCTTACGCAAGAGATCGTGTGCTGCTGCGGCGCAAGGTGACTTACAGGGA 933  
658 ATGTTCTCTAAGCTTTCTTCTCCCGTTAGAGATGCAAGCGGAGAGAGAGACGCT 717

934 ATGTTCTCTAAGCTTTCTTCTCCCGTTAGAGATGCAAGCGGAGAGAGAGACGCT 993  
718 GTCAAGAGTTCATCTCCAGGAGTGGCAGACTCCAGGCTCGGTGACGAGATCATG 777  
994 GTCAAGAGTTCATCTCCAGGAGTGGCAGACTCCAGGCTCGGTGACGAGATCATG 1053  
778 TCCGACCAAGAAAGCTGTTGTTATCATTAAGCGTTTCCATGACCTGGGCTCTGCTC 837  
1054 TCCGACCAAGAAAGCTGTTGTTATCATTAAGCGTTTCCATGACCTGGGCTCTGCTC 1113  
838 AACATGACCAAAAGCTCTGCAAGAGCTGGGCTGAGAGAGAGCTCCGTTCAACCTCATA 897  
1114 AACATGACCAAAAGCTCTGCAAGAGCTGGGCTGAGAGAGAGCTCCGTTCAACCTCATA 1173  
898 GCGAGTCTGTAAGAGAGTCTGCTCCCTGAGTCTCTTCTGATCGTCAACCGTCAGAGAC 957  
1174 GCGAGTCTGTAAGAGAGTCTGCTCCCTGAGTCTCTTCTGATCGTCAACCGTCAGAGAC 1233  
958 GTGGGCAAGAGAGTCTCAAGTCAAGAGTGTGCTCCCGTTACCTGTTAGTGAAGA 1017  
1234 GTGGGCAAGAGAGTCTCAAGTCAAGAGTGTGCTCCCGTTACCTGTTAGTGAAGA 1293  
1018 ATCTCCGGGGAACAAAGATTCATTGCTCTTGAAGCGGAGATTGGTAGCATCAGAAAG 1077  
1294 ATCTCCGGGGAACAAAGATTCATTGCTCTTGAAGCGGAGATTGGTAGCATCAGAAAG 1353  
1078 ACAAGAGGTTGCGTGCATCATGAAACAAGTGAAGTGTCTGACCAAGTGCAGAGTCCC 1137  
1354 ACAAGAGGTTGCGTGCATCATGAAACAAGTGAAGTGTCTGACCAAGTGCAGAGTCCC 1413  
1138 GCGGTGGCTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197  
1414 GCGGTGGCTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1473  
1198 GCGGTGGCTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257  
1474 GCGGTGGCTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1533  
1258 CCTGAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317  
1534 CCTGAGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1593  
1318 TGCCGTATGCTGTGAGAGAGTGTGAATGGAATGCAAGTGTGATGATGAGACCTC 1377  
1594 TGCCGTATGCTGTGAGAGAGTGTGAATGGAATGCAAGTGTGATGATGAGACCTC 1653  
1378 ATGTTTCAAGGACCTCGGAGTCTGAGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437  
1654 ATGTTTCAAGGACCTCGGAGTCTGAGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1713  
1438 CCAGACAGCACTGTGAGAGTACTACACTTCTTCCACTCAAGTCTCAAGACTTCTGCT 1497  
1714 CCAGACAGCACTGTGAGAGTACTACACTTCTTCCACTCAAGTCTCAAGACTTCTGCT 1773  
1498 GCGGCTTTGTACTACGTTTGAAGAGGCTGGAATTCAGACCAAGCTCTGCTGCTGCTG 1557  
1774 GCGGCTTTGTACTACGTTTGAAGAGGCTGGAATTCAGACCAAGCTCTGCTGCTGCTG 1833  
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1618 TGATGAAGCGTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1677  
1894 TGATGAAGCGTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1953  
1678 CTGCTGAGCTGTCCGTTCCCTGAGGAGTGAAGCAAGCTTCTGCACTGGGCTCTCTG 1737  
1954 CTGCTGAGCTGTCCGTTCCCTGAGGAGTGAAGCAAGCTTCTGCACTGGGCTCTCTG 2013  
1738 TTGGGTGAGAGCTTAATGCAACAACCCAGAGAGACCTCTGAGCGCTTCCACTGCTT 1797  
2014 TTGGGTGAGAGCTTAATGCAACAACCCAGAGAGACCTCTGAGCGCTTCCACTGCTT 2073

QY 1798 TTGAGACTCAGACAAAGAGTTTGTGCTTGAGATTAAAGCTTCCAGAAAGTGTGG 1857  
 Db 2074 TTGAGACTCAGACAAAGAGTTTGTGCTTGAGATTAAAGCTTCCAGAAAGTGTGG 2133  
 QY 1858 CTTCCGATTAAACCAAGACCTTGACCTTGATAGCATCTTCTTCTGCTCCAGACCTGTCCG 1917  
 Db 2134 CTTCCGATTAAACCAAGACCTTGACCTTGATAGCATCTTCTTCTGCTCCAGACCTGTCCG 2193  
 QY 1918 TATTTGCGGAAAATTCGGGTGGAATGTCAAAGGAACTTCCCAAGAGATGACCTGCTAG 1977  
 Db 2194 TATTTGCGGAAAATTCGGGTGGAATGTCAAAGGAACTTCCCAAGAGATGACCTGCTAG 2253  
 QY 1978 GCATGCTCTGTGCTCTCTATGATGCGGATTAAGACCTCTATTGAGAGAGTGGGA 2037  
 Db 2254 GCATGCTCTGTGCTCTCTATGATGCGGATTAAGACCTCTATTGAGAGAGTGGGA 2313  
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 Db 2314 GATTTCTGCTCCATGCTTGAGCAACCAACCACTGCGGACCTGGAACCTGCGGACGAC 2373  
 QY 2098 ATCCGAGAGAGCGGCGCATGAAAGACCTGTGTGCAAGCTGAGGCACTCCGCTGCAAG 2157  
 Db 2374 ATCCGAGAGAGCGGCGCATGAAAGACCTGTGTGCAAGCTGAGGCACTCCGCTGCAAG 2433  
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 Db 2434 ATACAGACCTCTGATGTTAGAAATGACAGATTACCCCTGTGTGAGAGACCTTGAGGA 2493  
 QY 2218 ATCCGATGAGCCCAACCGTAACCTTAAGATCCCTCAATTGAGAGGACCACTGAGGA 2277  
 Db 2494 ATCCGATGAGCCCAACCGTAACCTTAAGATCCCTCAATTGAGAGGACCACTGAGGA 2553  
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 Db 2554 GAGATGTAAGATGAGCGGTGTAAGCTTTAAAGACCCAAAATGTTTGTGAGAGCTTTG 2613  
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 Db 2614 AGGCTGATGCTGTGATGATGACCCATGCTGTACTGAGATCTCCAAATCTTTAG 2673  
 QY 2398 ACCCTCCCAAGCTGAAATCTCTGAGCTGTGAGGAAACAGGTGACAGACCAAGGAGTA 2457  
 Db 2674 ACCCTCCCAAGCTGAAATCTCTGAGCTGTGAGGAAACAGGTGACAGACCAAGGAGTA 2733  
 QY 2458 ATGCTCTCAGTATGCTTGAAGATCTTCCAGTGTGCGCTGCAAGAGCTGATCTGAG 2517  
 Db 2734 ATGCTCTCAGTATGCTTGAAGATCTTCCAGTGTGCGCTGCAAGAGCTGATCTGAG 2793  
 QY 2518 GACTGTGATCAACGACGAGGTTGCAAGAGTCTGAGCTCAAGCCCTGTCAGCAACCGG 2577  
 Db 2794 GACTGTGATCAACGACGAGGTTGCAAGAGTCTGAGCTCAAGCCCTGTCAGCAACCGG 2853  
 QY 2578 AGCTTGACACACTGTGCTTCAACCAAGCTGAGGAAACGAAGTGTAAATCTACTG 2637  
 Db 2854 AGCTTGACACACTGTGCTTCAACCAAGCTGAGGAAACGAAGTGTAAATCTACTG 2913  
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 QY 2758 CACCTGAGCCTTAGCATGAACCTGTGGAAGCAATGAGCTGAGAGCTTCTGTGAGAGTGC 2817  
 Db 3034 CACCTGAGCCTTAGCATGAACCTGTGGAAGCAATGAGCTGAGAGCTTCTGTGAGAGTGC 3093  
 QY 2818 ATGAGAGAACCAATCTTGTATCTCAAGACCTGAGGTTGTAAGTGTATCTACCGCC 2877  
 Db 3094 ATGAGAGAACCAATCTTGTATCTCAAGACCTGAGGTTGTAAGTGTATCTACCGCC 3153

QY 2878 GCGTCTGTGAGAGTCTGTCTGTGTGATCTTGAAGACAGACACTGTAAGAGCTTGAT 2937  
 Db 3154 GCGTCTGTGAGAGTCTGTCTGTGTGATCTTGAAGACAGACACTGTAAGAGCTTGAT 3213  
 QY 2938 CTCACGACCAATGCTTGTGTGAGAGCTGTGTGTGCTGTGTGTGCTGTGTGTGCTGTGTGTG 2997  
 Db 3214 CTCACGACCAATGCTTGTGTGAGAGCTGTGTGTGCTGTGTGTGCTGTGTGTGCTGTGTGTG 3273  
 QY 2998 AAGAACAGTGTCTGACAGAGCTGTGTGTGAGAGGATGAGCTGATCTTGAATGCTGT 3057  
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 QY 3058 GAGGCACTCTCTGCTGCTTCTCTGCAACCGGACCTGACAGCTTAACCTGTGTGAG 3117  
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 QY 3178 AACTTACAGATTAATGAGCTGTGGAATGAGAGTACCTGTCGCAATTAAGAAAGTGTGCT 3237  
 Db 3454 AACTTACAGATTAATGAGCTGTGGAATGAGAGTACCTGTCGCAATTAAGAAAGTGTGCT 3513  
 QY 3238 GAGGAAGTGAAGTACTCAAGCCCGAGTGTGATTAAGAGTGTGAGCTTCTTTGAT 3297  
 Db 3514 GAGGAAGTGAAGTACTCAAGCCCGAGTGTGATTAAGAGTGTGAGCTTCTTTGAT 3573  
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 Db 3574 GAGGATGACCGGTAC 3588

RESULT 4  
 US-10-399-443-23  
 ; Sequence 23, Application US/10399443  
 ; Publication No. US2004028669A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Government of the United States of America, as Represented by the  
 ; APPLICANT: Secretary, Department of Health & Human Services, The National Institute  
 ; APPLICANT: Health  
 ; APPLICANT: Nelson, Lawrence M.  
 ; APPLICANT: Tong, Zhi-Bin  
 ; APPLICANT: Nelson, Lawrence  
 ; APPLICANT: Zhi-Bin, Tong  
 ; TITLE OF INVENTION: Human Gene Critical to Fertility  
 ; FILE REFERENCE: 4239-64785  
 ; CURRENT APPLICATION NUMBER: US/10/399,443  
 ; PRIOR FILING DATE: 2003-04-16  
 ; PRIOR APPLICATION NUMBER: 60/241,510  
 ; PRIOR FILING DATE: 2000-10-18  
 ; PRIOR APPLICATION NUMBER: PCT/US01/10981  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 23  
 ; LENGTH: 3900  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3600)  
 ; OTHER INFORMATION:  
 ; US-10-399-443-23

Query Match 78.5%; Score 3166.2; DB 17; Length 3900;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;

QY 1 ATGAGAGAGCAAAATGCTCACTTTTCAAGTACGAGGCTGCAATGCTGTCTATGAG 60  
 Db 154 ATGAGAGAGCAAAATGCTCACTTTTCAAGTACGAGGCTGCAATGCTGTCTATGAG 213

QY 61 CTGACAGAGAAATTTCAAGCATTCAAGAAATTACTAAAGAGAAATCTTCAGAAATCG 120  
Db 214 CTAGCAAGAGAAATTTCAAGCATTCAAGAAATTACTAAAGAGAAATCTTCAGAAATCG 273  
QY 121 ACCCAATGCTATTTCCACAGTTTGAATTCAGAAATTCGAAATGTCGTGCAATTC 180  
Db 274 ACCCAATGCTATTTCCACAGTTTGAATTCAGAAATTCGAAATGTCGTGCAATTC 333  
QY 181 CTCTGCAATGATTTATGAGCATCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 240  
Db 334 CTCTGCAATGATTTATGAGCATCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 393  
QY 241 AACATGAACCTGCGAACCTCTCGGAGAGGCAAGGATGACATGAAAA----- 289  
Db 394 AACATGAACCTGCGAACCTCTCGGAGAGGCAAGGATGACATGAAAAATTCACCA 453  
QY 290 ----- 289  
Db 454 GAAATCTCTGAAGCAAGATGACTGACCAAGAGCAAGCAAGAAAAATGCGCAGGAATT 513  
QY 290 -----AATTTCA 297  
Db 514 TCACAGCTGTGCAACAGATAGTGCACAGCTGACAGACAAAAGAACAGGAATTTCA 573  
QY 298 CAAGCTATGAAACAAAGAGTGCACAGCAGACAGACAGACAAAGAAATTTCA 357  
Db 574 CAAGCTATGAAACAAAGAGTGCACAGCAGACAGACAGACAAAGAAATTTCA 633  
QY 358 GCTATGAAACAAAGAGTGCACAGCAGACAGACAGACAAAGAAATTCAGAGGTAC 417  
Db 634 GCTATGAAACAAAGAGTGCACAGCAGACAGACAGACAAAGAAATTCAGAGGTAC 693  
QY 418 ACATGAGGACTCAAGAGTCAAGTATGACCAAAATTCGCTGAGAGAGAGATGACGTCT 477  
Db 694 ACATGAGGACTCAAGAGTCAAGTATGACCAAAATTCGCTGAGAGAGAGATGACGTCT 753  
QY 478 AGTTTGAACCACTGCTGTGACTGCTGCGGAAATGCAACGTTGCTGCTTTGAT 537  
Db 754 AGTTTGAACCACTGCTGTGACTGCTGCGGAAATGCAACGTTGCTGCTTTGAT 813  
QY 538 TCAGACCGGTGGGGCTTCGCGCTTCGCAAGGTGTTTCGCAAGGAAATTCAGAAATTCGG 597  
Db 814 TCAGACCGGTGGGGCTTCGCGCTTCGCAAGGTGTTTCGCAAGGAAATTCAGAAATTCGG 873  
QY 598 AAATGAGCTTACAGAGAGATCGTGTGCTGAGGCGCAAGGTGACTTACCAAGGGA 657  
Db 874 AAATGAGCTTACAGAGAGATCGTGTGCTGAGGCGCAAGGTGACTTACCAAGGGA 933  
QY 658 ATGTTCTCTACGTTCTTCTCTCCGTTAGAGATGCAAGCGGAGAGAGAGAGAGT 717  
Db 934 ATGTTCTCTACGTTCTTCTCTCCGTTAGAGATGCAAGCGGAGAGAGAGAGAGT 993  
QY 718 GTCACAGATTCATTCAGAGAGTGCACATCCAGGCTCCGAGTACCGGAGTAC 777  
Db 994 GTCACAGATTCATTCAGAGAGTGCACATCCAGGCTCCGAGTACCGGAGTAC 1053  
QY 778 TCCGACCAAGAAAGCTGTTGTTCAATTCATTCAGTTCGTTGATGACCTGAGCTGCTC 837  
Db 1054 TCCGACCAAGAAAGCTGTTGTTCAATTCATTCAGTTCGTTGATGACCTGAGCTGCTC 1113  
QY 838 AACCAATGACAAAGCTTCGCAAGAGCTGGGCTGAGAGAGAGAGAGAGAGTCCCTCA 897  
Db 1114 AACCAATGACAAAGCTTCGCAAGAGCTGGGCTGAGAGAGAGAGAGAGAGTCCCTCA 1173  
QY 898 CGCAGTCTGCTGAGAGAGTCTGCTCCCTGAGTCTTCTGATGATGATGATGATGATGAT 957  
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QY 1018 ATCTCCGGGGAACAAAGATCCACTTGTCTCTTGAAGCGGAGATTGATGACATCAAG 1077

Db 1294 ATCTCCGGGGAACAAAGATCCACTTGTCTCTTGAAGCGGAGATTGATGACATCAAG 1353  
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QY 1138 GCGGTGGGCTCTCATCTGCGTGGCCCTGACAGTGCAGAGAGAGAGAGAGAGTCC 1197  
Db 1414 GCGGTGGGCTCTCATCTGCGTGGCCCTGACAGTGCAGAGAGAGAGAGAGAGTCC 1473  
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Db 1474 GCCCCTTTCAACCAAGGCTCAAGGCTGACAGCCGCTTTGTTGTTTCACTACACC 1533  
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Db 1534 CCTGAGAGGCTGTCGCGGCTGCTCAATCTGAGAGAGAGAGAGAGAGTTCCTGAAGCTTC 1593  
QY 1318 TGCCGTATGCTGTGAGAGAGTGTGAATAGAAATGAGTTCAGTGTGATGATGACCTC 1377  
Db 1594 TGCCGTATGCTGTGAGAGAGTGTGAATAGAAATGAGTTCAGTGTGATGATGACCTC 1653  
QY 1378 ATGTTCAAGAGCTTCGAGAGTCTGAGTCCGTCTCTGTTTCAATGAACATCTTCTC 1437  
Db 1654 ATGTTCAAGAGCTTCGAGAGTCTGAGTCCGTCTCTGTTTCAATGAACATCTTCTC 1713  
QY 1438 CCAGACAGCCACTGTGAGAGTACTACACCTTCTTCAACCTCACTCCAGAGCTTCTGT 1497  
Db 1714 CCAGACAGCCACTGTGAGAGTACTACACCTTCTTCAACCTCACTCCAGAGCTTCTGT 1773  
QY 1498 GCCGCTTTGTACTACGTGTTAGAGAGGCTGTGAATTCAGAGGCTCTGCTCTGTAC 1557  
Db 1774 GCCGCTTTGTACTACGTGTTAGAGAGGCTGTGAATTCAGAGGCTCTGCTCTGTAC 1833  
QY 1558 GTTGAAGAGCAAGAGTCCATGAGCTTAAACAGGAGCTTCCATATCTGCTT 1617  
Db 1834 GTTGAAGAGCAAGAGTCCATGAGCTTAAACAGGAGCTTCCATATCTGCTT 1893  
QY 1618 TGAATGAAGGCTTCTTGTGCTGCTGCTGAGAGAGAGTTCAGAGAGGCTCAAGAGTTC 1677  
Db 1894 TGAATGAAGGCTTCTTGTGCTGCTGAGAGAGAGTTCAGAGAGGCTCAAGAGTTC 1953  
QY 1678 CTGCTGGGCTGTCCGTTCCCTGAGGAGTGAAGCAAGCTTTCAGCTGGGTCTCTCTG 1737  
Db 1954 CTGCTGGGCTGTCCGTTCCCTGAGGAGTGAAGCAAGCTTTCAGCTGGGTCTCTCTG 2013  
QY 1738 TTGGGTGAGAGGCTTAATGCGACACACCCAGAGAGACACCTGAGAGGCTTCTGCTT 1797  
Db 2014 TTGGGTGAGAGGCTTAATGCGACACACCCAGAGAGACACCTGAGAGGCTTCTGCTT 2073  
QY 1798 TTGAGACTCAAGCAAGAGTGTGTTGCTTGGCTTTAAACAGCTTCAAGAGTGTG 1857  
Db 2074 TTGAGACTCAAGCAAGAGTGTGTTGCTTGGCTTTAAACAGCTTCAAGAGTGTG 2133  
QY 1858 CTTCCGATTAACAGAACTTGAGCTTATGATCATCTTCTGCTCCAGAGCTGTCCG 1917  
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QY 1918 TATTTGGGAAAAATTCGAGTGAATGTCAGAGAGATCTTCCAGAGATGATGATGATGAT 1977  
Db 2194 TATTTGGGAAAAATTCGAGTGAATGTCAGAGAGATCTTCCAGAGATGATGATGATGAT 2253  
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Db 2254 GCATGCTGTGTCCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2133  
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Db 2214 GATTTCTGCTCATGCTTGGGACCAACCACTGCGGAGCTGAGACTTGGGAGAGAGC 2373  
QY 2098 ATCTGACAGAGCGGACATGAGAGCCCTGTGTCCAGAGTGAAGCATCCACTGCAAG 2157

Db 2374 ATCTGACAGAGCGGCGCATGAAAGCCTGTGTGCCAAGCTGAGGCTCCAGCTGCAAG 2433  
Qy 2158 ATACAGACCTCTGATTTTGAAGATGACAGATTAACCCCTGTGTGAGGACCTCTGAGAA 2217  
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Qy 2218 ATCTGATGAGGCAACCTGTAACCTTAAGATCCCTCAACCTTGGAGGACCCAGCTGAAGAA 2277  
Db 2494 ATCTGATGAGGCAACCTGTAACCTTAAGATCCCTCAACCTTGGAGGACCCAGCTGAAGAA 2553  
Qy 2278 GAGGATGTAAGATGAGGCTGTGTAAGCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2337  
Db 2554 GAGGATGTAAGATGAGGCTGTGTAAGCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2613  
Qy 2338 AGGCTGATGCTGTGATGTAAGCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2397  
Db 2614 AGGCTGATGCTGTGATGTAAGCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2673  
Qy 2398 AACTCCCCAGCTGTAATCTCTGAGCTGCGAGGAAACAGAGTGAAGAGAGGAGTA 2457  
Db 2674 AACTCCCCAGCTGTAATCTCTGAGCTGCGAGGAAACAGAGTGAAGAGAGGAGTA 2733  
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Db 2734 AAGCTCTGATGATGCTGTAAGCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2793  
Qy 2518 GACTGTGATGATGATGCTGTAAGCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2577  
Db 2794 GACTGTGATGATGATGCTGTAAGCTTAAACCCCAAAATGTTTGTGAGTCTTGG 2853  
Qy 2578 AGCTTGACACCTGTGCTTATCAACACAGCTGCGGAGGAAAGAGTGAATCTACTG 2637  
Db 2854 AGCTTGACACCTGTGCTTATCAACACAGCTGCGGAGGAAAGAGTGAATCTACTG 2913  
Qy 2638 TGTGATCATGAGGCTTCCCACTGTAAGCTGTAAGCTGTAAGCTGTAAGCTGTAAG 2697  
Db 2914 TGTGATCATGAGGCTTCCCACTGTAAGCTGTAAGCTGTAAGCTGTAAGCTGTAAG 2973  
Qy 2698 CTGACAGGCTGCTGTGTGTTTCTTGTGACCTTGTGAGGCTTGTGAGGCTGTAAG 2757  
Db 2974 CTGACAGGCTGCTGTGTGTTTCTTGTGACCTTGTGAGGCTTGTGAGGCTGTAAG 3033  
Qy 2758 CACCTGACCTTGAATGACCTCTGTGAGGACCAATGCGGTGAAGCTTGTGAGGAGT 2817  
Db 3034 CACCTGACCTTGAATGACCTCTGTGAGGACCAATGCGGTGAAGCTTGTGAGGAGT 3093  
Qy 2818 ATGAGAGAACCACTTGTGATCTGAGGACCTGAGAGTGAAGTGTGATCTGACCGC 2877  
Db 3094 ATGAGAGAACCACTTGTGATCTGAGGACCTGAGAGTGAAGTGTGATCTGACCGC 3153  
Qy 2878 GCGTCTGTGAGAGTCTGTCTGTGTGATCTGAGAGGACCACTGTAAGGCTGTGAT 2937  
Db 3154 GCGTCTGTGAGAGTCTGTCTGTGTGATCTGAGAGGACCACTGTAAGGCTGTGAT 3213  
Qy 2938 CTGACAGCAATGCGCTGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2997  
Db 3214 CTGACAGCAATGCGCTGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3273  
Qy 2998 AAGAACAGTGTGTAAGGACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3057  
Db 3274 AAGAACAGTGTGTAAGGACCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 3333  
Qy 3058 GAGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3117  
Db 3334 GAGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3393  
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Db 3394 AATACTCAAGTCCCAAGAGATGATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 3453  
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Db 3454 AACTTACAGATTAATGAGCTGTGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCT 3513

Qy 3238 GAGGAGTGCAGCTACTCAAGCCCGAGTGTGATGAGGCTGATGCTGATGCTGATGAT 3297  
Db 3514 GAGGAGTGCAGCTACTCAAGCCCGAGTGTGATGAGGCTGATGAGGCTGATGATGAT 3573  
Qy 3298 GAGGAGTGCAGCTACTCAAGCCCGAGTGTGATGAGGCTGATGAGGCTGATGAT 3312  
Db 3574 GAGGAGTGCAGCTACTCAAGCCCGAGTGTGATGAGGCTGATGAGGCTGATGAT 3588

RESULT 5  
US-10-677-943-23  
; Sequence 23, Application US/10677943  
; Publication No. US20040072297A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America as  
; APPLICANT: represented by the Secretary of the Department of Health and  
; APPLICANT: Human Services  
; APPLICANT: Nelson, Lawrence  
; APPLICANT: Tong, Zhi-Bin  
; TITLE OF INVENTION: Human Gene Critical to Fertility  
; FILE REFERENCE: 4239-64790  
; CURRENT APPLICATION NUMBER: US/10/677,943  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: 60/241,510  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: PCT/US02/09776  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: PCT/US01/10981  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 23  
; LENGTH: 3900  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3600)  
US-10-677-943-23

Query Match 78.5%; Score 316.2; DB 17; Length 3900;  
Best Local Similarity 96.2%; Pred. No. 0;  
Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;

Qy 1 ATGAGAGAGACAAATCCCTGACCTTTTCAGCTACGCGGCTGCAATGCTGCTATGAG 60  
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Db 214 CTAGACAGAGAAATTTTCAAGCAATTCAGAAATTAAGAAATCTTCAAGATCG 273  
Qy 121 ACCACATCTCTATTCACAGATTTGAATGCAAGATGCAAGATGCTGCACTC 180  
Db 274 ACCACATCTCTATTCACAGATTTGAATGCAAGATGCAAGATGCTGCACTC 333  
Qy 181 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
Db 334 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 393  
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Qy 290 ----- 289  
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Qy 290 -----AATTTC 297  
Db 514 TCACAGCTGTGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 573

QY 298 CAAGCTATGAAACAAGAGTGGCCACAGCAGCAGAGACAGAAACAAGAAATTTACAA 357  
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QY 574 CAAGCTATGAAACAAGAGTGGCCACAGCAGCAGAGACAGAAACAAGAAATTTACAA 633  
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QY 358 GCTATGAAACAAGAGTGGCCACAGCAGCAGAGACAGAAACAAGCATGGAGTGC 417  
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QY 418 ACATGGAGCTACAGAGTCAAGTATGACAAATTCGCTGAGAGAGATGTACGTGCT 477  
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QY 754 AGTTTGAACAACCTGCTGACCTGGCCGGAATGCAACGTTGGCTGTTGAT 813  
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Db |||||  
QY 814 TCAGACCGGTGGGGCTTCGGGCTTCGACCGGTGTTGCAACGGAATGCAAGAAATTGGG 873  
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QY 658 ATGTTCTCTACGTTCTTCTCCCGTTAGAGATGCAAGCGGAAGAGAGACGT 717  
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QY 718 GTCAAGAGTTCATTCGAGGAGTGGGCAATCCGAGGCTCCGGTGAACGAATCATG 777  
Db |||||  
QY 994 GTCAAGAGTTCATTCGAGGAGTGGGCAATCCGAGGCTCCGGTGAACGAATCATG 1053  
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QY 1054 TCCGACCAAGAAAGGCTGTGTCATCATGACGTTTCAGTACCTGGGCTGTGCTC 1113  
Db |||||  
QY 838 AACATGACACAAGACTCTGCAAGAATGGGCTGAGAGACGCTCCGTTACCTCAT 897  
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QY 1114 AACATGACACAAGACTCTGCAAGAATGGGCTGAGAGACGCTCCGTTACCTCAT 1173  
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QY 898 CGCAGTCTGAGGAGAGTCTGTGCTCCGTAAGCTTCGATGTCACGTCAGAAC 957  
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QY 1174 CGCAGTCTGAGGAGAGTCTGTGCTCCGTAAGCTTCGATGTCACGTCAGAAC 1233  
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QY 958 GTGGGACAGAGAAAGCTCAAGTCAAGAGTCCGTTACCTCCGTTACCTGTTAGAGA 1017  
Db |||||  
QY 1234 GTGGGACAGAGAAAGCTCAAGTCAAGAGTCCGTTACCTCCGTTACCTGTTAGAGA 1293  
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QY 1018 ATCTCCGGGAAACAAGAAATCACTTGTCTTGAAGCGGGATTTGTAGCATCAGAA 1077  
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QY 1078 ACACAAGGTTGGTGGCATCATGAACAACGTTAGAGTCTGACCAATGCGAGTGC 1137  
Db |||||  
QY 1354 ACACAAGGTTGGTGGCATCATGAACAACGTTAGAGTCTGACCAATGCGAGTGC 1413  
Db |||||  
QY 1138 GCCGTGGGCTCTCATCTGAGTGGCCCTGACGCTGACAGAGTGGTGGGGAGAGCTC 1197  
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QY 1414 GCCGTGGGCTCTCATCTGAGTGGCCCTGACGCTGACAGAGTGGTGGGGAGAGCTC 1473  
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QY 1198 GCCCCCTTCAACAACGCTCAACAGGCTGACCGCCGCTTTTGTGTTTCATCACTCA 1257  
Db |||||  
QY 1474 GCCCCCTTCAACAACGCTCAACAGGCTGACCGCCGCTTTTGTGTTTCATCACTCA 1533  
Db |||||  
QY 1258 CCTGAGAGGCTGGTCCGCGCTGTCTCAATCTGAGAGAAAGATTGTCTGAAGGCTTC 1317  
Db |||||  
QY 1534 CCTGAGAGGCTGGTCCGCGCTGTCTCAATCTGAGAGAAAGATTGTCTGAAGGCTTC 1593  
Db |||||  
QY 1318 TGCCGATATGAGCTGAGAGAGTGAATGAATGAAGTCAAGTGTGTTGATGAGTGAAGCTC 1377  
Db |||||  
QY 1594 TGCCGATATGAGCTGAGAGAGTGAATGAATGAAGTCAAGTGTGTTGATGAGTGAAGCTC 1653  
Db |||||  
QY 1378 ATGCTTCAAGAGCTTCGGGAGTCTGAGCTCCGTGCTGTGTTCAATGAAATCCTTCTC 1437  
Db |||||

Db |||||  
QY 1554 ATGCTTCAAGAGCTTCGGGAGTCTGAGCTCCGTGCTGTGTTCAATGAATATCTTCTC 1713  
Db |||||  
QY 1438 CCAGACAGCCACTGTGAGAGTACTACACTTCTTCCACTCAAGTCTCAGACTTCTGT 1497  
Db |||||  
QY 1714 CCAGACAGCCACTGTGAGAGTACTACACTTCTTCCACTCAAGTCTCAGACTTCTGT 1773  
Db |||||  
QY 1498 GCCGCTTGTATCTACGTTTGAAGAGGCTTGAAATTCAGACCAAGCTCTCTGCTGTAC 1557  
Db |||||  
QY 1774 GCCGCTTGTATCTACGTTTGAAGAGGCTTGAAATTCAGACCAAGCTCTCTGCTGTAC 1833  
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QY 1558 GTTGAAGAGCAAGAGTCCATGAGCTTAAACAGGACGCTTCCATATCCACTCCTT 1617  
Db |||||  
QY 1834 GTTGAAGAGCAAGAGTCCATGAGCTTAAACAGGACGCTTCCATATCCACTCCTT 1893  
Db |||||  
QY 1618 TGGATGAAGCGTTCTTGTGAGCCTGATGACGAACGTTAAGAGAGCCACTGAGAGTC 1677  
Db |||||  
QY 1894 TGGATGAAGCGTTCTTGTGAGCCTGATGACGAACGTTAAGAGAGCCACTGAGAGTC 1953  
Db |||||  
QY 1678 CTGCTGGGCTGTCCGTTCCCTGGGAGTGAAGCAAGCTTTCGACTGAGCTCTCTG 1737  
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QY 1954 CTGCTGGGCTGTCCGTTCCCTGGGAGTGAAGCAAGCTTTCGACTGAGCTCTCTG 2013  
Db |||||  
QY 1738 TTGGGTCAGAGCCTTAATGCAACCACTCCAGAGACACCTTGGACGCTTCCACTGTCT 1797  
Db |||||  
QY 2014 TTGGGTCAGAGCCTTAATGCAACCACTCCAGAGACACCTTGGACGCTTCCACTGTCT 2073  
Db |||||  
QY 1798 TTGAGACTCAAGCAAGAGTTGTTGAGCTGGCACTTAAACAGCTTCCAAAGATGTGG 1857  
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QY 2074 TTGAGACTCAAGCAAGAGTTGTTGAGCTGGCACTTAAACAGCTTCCAAAGATGTGG 2133  
Db |||||  
QY 1858 CTTCCGATTAACAAGAACTGGAACCTTATGACATCTTCTGTGCTTCAGACCTGTCCG 1917  
Db |||||  
QY 2134 CTTCCGATTAACAAGAACTGGAACCTTATGACATCTTCTGTGCTTCAGACCTGTCCG 2193  
Db |||||  
QY 1918 TATTTGGGAAAAATTCGGGATGATGTCAAGAGATCTTCCCAAGATGAGTCCGCTGAG 1977  
Db |||||  
QY 2194 TATTTGGGAAAAATTCGGGATGATGTCAAGAGATCTTCCCAAGATGAGTCCGCTGAG 2253  
Db |||||  
QY 1978 GCATGCTCTGTGTCCTCTTATGAGTCCGGATTAAGACCTTCATTGAGAGCACTGGGAA 2037  
Db |||||  
QY 2254 GCATGCTCTGTGTCCTCTTATGAGTCCGGATTAAGACCTTCATTGAGAGCACTGGGAA 2133  
Db |||||  
QY 2038 GATTTGCTTCATGCTTGGGACCCACCACTTCGCGGACGTGACCTTGGGACGAGC 2097  
Db |||||  
QY 2214 GATTTGCTTCATGCTTGGGACCCACCACTTCGCGGACGTGACCTTGGGACGAGC 2373  
Db |||||  
QY 2098 ATCTGACAGAGCGGCGCATGAAAGACCTGTGTGCCAAGCTGAGGATCCCACTGCAAG 2157  
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QY 2374 ATCTGACAGAGCGGCGCATGAAAGACCTGTGTGCCAAGCTGAGGATCCCACTGCAAG 2433  
Db |||||  
QY 2158 ATACAGACCCGTAGTTTAAAGATGCAAGATTACCCCTGGTGGAGCACTCTGAGAA 2217  
Db |||||  
QY 2434 ATACAGACCCGTAGTTTAAAGATGCAAGATTACCCCTGGTGGAGCACTCTGAGAA 2493  
Db |||||  
QY 2218 ATCTGATAGGCAACCGTTAACCTTAAGATCCCTCAACTTGGAGGCAACCACTGAGAAA 2277  
Db |||||  
QY 2494 ATCTGATAGGCAACCGTTAACCTTAAGATCCCTCAACTTGGAGGCAACCACTGAGAAA 2553  
Db |||||  
QY 2278 GAGGATGTAAGATGGGTGTGAAGCTTAAACCAACCAAAATTTGTTGAGATCTTTG 2337  
Db |||||  
QY 2554 GAGGATGTAAGATGGGTGTGAAGCTTAAACCAACCAAAATTTGTTGAGATCTTTG 2613  
Db |||||  
QY 2238 AGGCTGAATTGCTGTGATGGAACCATAGCCTGTTACCTGAAGATCTCCCAAATCTTAAG 2397  
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QY 2614 AGGCTGAATTGCTGTGATGGAACCATAGCCTGTTACCTGAAGATCTCCCAAATCTTAAG 2673  
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QY 2398 ACTTCCCCAGCCTGAATCTCTGAGCCTGGCAGAGAAACAAGTGAAGACCAAGGAGTA 2457  
Db |||||  
QY 2674 ACTTCCCCAGCCTGAATCTCTGAGCCTGGCAGAGAAACAAGTGAAGACCAAGGAGTA 2733  
Db |||||  
QY 2458 ATGCTTCAAGTATGCTTGAAGATCTCCAGTGGCCCTGCAAGAGCTGATCTGAGAG 2517  
Db |||||



Db	2734	AGCCTCTCAGTGAATGCTTGAAGGATCTCCAGTGCCTGACAGAAAGCTGATCTGAG	2733
Qy	2518	GACTGTGGCATTCACAGCCACGGGTTGCCAGAGTCTGGCTCAGCCCTGTCAAGCAACCG	2577
Db	2794	GACTGTGGCATTCACAGCCACGGGTTGCCAGAGTCTGGCTCAGCCCTGTCAAGCAACCG	2853
Qy	2578	AGCTTGAACAACCTGTGCTTATCCAAACAACAGCCTGGGGAAAGAGTGTAAATCTAC	2637
Db	2854	AGCTTGAACAACCTGTGCTTATCCAAACAACAGCCTGGGGAAAGAGTGTAAATCTAC	2913
Qy	2638	TGTGCATCCATGAGGCTTCCCACCTGATGTCGAGAGGCTGATGCTGAATCAATGCCAC	2697
Db	2914	TGTGCATCCATGAGGCTTCCCACCTGATGTCGAGAGGCTGATGCTGAATCAATGCCAC	2973
Qy	2698	CTGGAACAAGGCTGGCTGATGTTCTTCCACTGTGGCTTATGGGGTAACTCAATGGCTGAG	2755
Db	2974	CTGGAACAAGGCTGGCTGATGTTCTTCCACTGTGGCTTATGGGGTAACTCAATGGCTGAG	3033
Qy	2758	CACCTGAGCCTTATGAGTGAACCTCTGTGGAAGACAATGCGTGAAGCTTCTGTGCGAGGTC	2817
Db	3034	CACCTGAGCCTTATGAGTGAACCTCTGTGGAAGACAATGCGTGAAGCTTCTGTGCGAGGTC	3093
Qy	2818	ATGAGAGAACCATCTTTCATCTCCAGGACTGGAAGTTGGTAAATGTCATCTCACCGCC	2877
Db	3094	ATGAGAGAACCATCTTTCATCTCCAGGACTGGAAGTTGGTAAATGTCATCTCACCGCC	3153
Qy	2878	GCGAGCTGTGAGAGTCTGCTCCTGTGTGATCTCGAGAGACAGACACTGAAGGCTGGAT	2937
Db	3154	GCGAGCTGTGAGAGTCTGCTCCTGTGTGATCTCGAGAGACAGACACTGAAGGCTGGAT	3213
Qy	2938	CTCACGGACAATGCCCTGGGTGACGGTGGGGTTCGTGCTGTGCGAGGGACTGAAGCA	2997
Db	3214	CTCACGGACAATGCCCTGGGTGACGGTGGGGTTCGTGCTGTGCGAGGGACTGAAGCA	3273
Qy	2998	AAGAACATGTCTCGACGACTGGGGTTGAAGGATGGAACCTTCTGATTTGCTG	3055
Db	3274	AAGAACATGTCTCGACGACTGGGGTTGAAGGATGGAACCTTCTGATTTGCTG	3333
Qy	3058	GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCACTGACCAAGCTTAAACCTGTGCAG	3117
Db	3334	GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCACTGACCAAGCTTAAACCTGTGCAG	3393
Qy	3118	AATAACTTCAAGTCCCAAGAAATGAAAGCTGTGTGGGCTTGTGCTGTGCCACGTCT	3177
Db	3394	AATAACTTCAAGTCCCAAGAAATGAAAGCTGTGTGGGCTTGTGCTGTGCCACGTCT	3453
Qy	3178	AACCTTACAGATTAATTGGGCTGTGAAAAAGGAGTACCTGTGCAAAATAAGAAAGTGTG	3237
Db	3454	AACCTTACAGATTAATTGGGCTGTGAAAAAGGAGTACCTGTGCAAAATAAGAAAGTGTG	3513
Qy	3238	GAGGAAGTGACCTACTCAAGCCCCGAGTGTGTAATTGAACGGTATGTGGCATTTCTTTGAT	3297
Db	3514	GAGGAAGTGACCTACTCAAGCCCCGAGTGTGTAATTGAACGGTATGTGGCATTTCTTTGAT	3573
Qy	3298	GAAGATGACCAACAC 3312	
Db	3574	GAAGATGACCGGTAC 3588	

RESULT 6  
US-10-216-645-3  
Sequence 3, Application US/10216645  
Publication No. US20030125282A1  
GENERAL INFORMATION:  
APPLICANT: WEISS, BERTRAM  
APPLICANT: LESSL, MONIKA  
APPLICANT: PETERS-KOTTIG, MICHAEL  
APPLICANT: BECKMANN, GEORG  
TITLE OF INVENTION: HUMAN WATER PROTEINS  
FILE REFERENCE: SCH-1910  
CURRENT APPLICATION NUMBER: US/10/216,645  
CURRENT FILING DATE: 2003-01-21  
PRIOR APPLICATION NUMBER: DE 101 39 874.3 411

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; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-10-216-645-3

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Query Match	77.8%	Score 3139;	DB 15;	Length 3830;
Best Local Similarity	96.0%;	Pred. No. 0;		
Matches 3282;	Conservative	0;	Mismatches 30;	Indels 105; Gaps 2,

QY	1	ATGGAAAGAGACA	AAATCGCTCA	CTTTTCACACTAC	CGGCTCGCAATG	GTGTC	CTA	ATGAG	60	
Db	1	ATGGAAAGAGACA	AAATCGCTCA	CTTTTTC	CACCTAC	CGGCTCGCAATG	GTGTC	CTA	ATGAG	60
QY	61	CTAGCAAGAGAA	GAATTTTCAG	CACTTCAAGAA	TTATCTA	AAAGAAATCTT	CAGAA	TG	120	
Db	61	CTAGCAAGAGAA	GAATTTTCAG	CATTCAAGAA	TTATCTA	AAAGAAATCTT	CAGAA	TG	120	
QY	121	ACCAATGCTCT	ATATTCAC	AGTTTGA	AAATCGAA	TGCGCAAGTGA	ATGTC	TGG	180	
Db	121	ACCAATGCTCT	ATATTCAC	AGTTTGA	AAATCGAA	TGCGCAAGTGA	ATGTC	TGG	180	
QY	181	CTTTTGCAT	TGAGTATTTA	TGAGCAATCG	CTGGCTCGGCTAC	CTCCATTTG	CAATCTTTTGA		240	
Db	181	CTTTTGCAT	TGAGTATTTA	TGAGCAATCG	CTGGCTCGGCTAC	CTCCATTTG	CAATCTTTTGA		240	
QY	241	AACATGAAC	TGCGAAAC	CTCTCGGAGAA	GGCAGCGGAATGA	CATGAGAAA	AAAAATTT	CACA	300	
Db	241	AACATGAAC	TGCGAAAC	CTCTCGGAGAA	GGCAGCGGAATGA	CATGAGAAA	AAAAATTT	CACA	300	
QY	301	GCT-----	ATGGAA	CAAGAGGTG	CCACAGCAG	CAGAGACAG	AAGAA	CA-	344	
Db	301	GATCTGA	AGCAAGATG	ATGATCGAC	CAAGAGACAG	AAGAA	AAAGTGC	CAGAA	360	
QY	345	-----	-----	-----	-----	-----	-----	-----	344	
Db	361	TATGGCAT	GACTTA	ATCTTGGGGGTG	TCGACATCT	CGACTCGAA	TATATA	CAC	420	
QY	345	-----	-----	AGAAATTT	CAACAGCTA	TGGAACA	GAAGGT		375	
Db	421	AAGTATGT	GGAATTCAT	TTCTTTTG	CAGAAATTT	CAACAGCTA	TGGAACA	GAAGGT	480	
QY	376	GCCA	CAGCAGCAG	AGAGACAG	AAGAA	CAAGAGCA	TGAGAGTGA	CAATG	435	
Db	481	GCCA	CAGCAGCAG	AGAGACAG	AAGAA	CAAGAGCA	TGAGAGTGA	CAATG	540	
QY	436	CA	CGTGAATGA	CCAA	TTGGCTG	AGAGAGATGA	TGACCTG	CTA	495	
Db	541	CA	CGTGAATGA	CCAA	TTGGCTG	AGAGAGATGA	TGACCTG	CTA	600	
QY	496	GCTG	ACTGGCGG	AAATGCA	AACTGTGGCTG	GTGCTTTG	TGATTCAGA	CCG	555	
Db	601	GCTG	ACTGGCGG	AAATGCA	AACTGTGGCTG	GTGCTTTG	TGATTCAGA	CCG	660	
QY	556	CGG	CTCGCA	CGGTG	TTCTG	CA	CGAA	AA	615	
Db	661	CGG	CTCGCA	CGGTG	TTCTG	CA	CGAA	AA	720	
QY	616	AGGA	TCGTCGTG	TGCTGG	CGCAAGTGA	CTCTAC	CAAGGA	AA	675	
Db	721	AGGA	TCGTCGTG	TGCTGG	CGCAAGTGA	CTCTAC	CAAGGA	AA	780	
QY	676	TTCT	CTCCCG	TTA	GAGATG	CAGCGG	AAAGAGAG	CA	735	
Db	781	TTCT	CTCCCG	TTA	GAGATG	CAGCGG	AAAGAGAG	CA	840	
QY	736	AGGA	GTGGCC	AGATCTCC	ACAGGCTCC	GTGACCG	AGATCA	AT	795	
Db	841	AGGA	GTGGCC	AGATCTCC	ACAGGCTCC	GTGACCG	AGATCA	AT	900	



Qy 796 TTGTTCAATGACGGTTTGATGACCTGGGCTGTGCTTCAACAATGACAACAAGCTC 855  
 Db 901 TTGTTCAATGACGGTTTGATGACCTGGGCTGTGCTTCAACAATGACAACAAGCTC 960  
 Qy 856 TGCAGAGCTGGGGTGAAGACAGCTCCGTTCAACCCCTATACGAGCTGTGTAGAGAG 915  
 Db 961 TGCAGAGCTGGGGTGAAGACAGCTCCGTTCAACCCCTATACGAGCTGTGTAGAGAG 1020  
 Qy 916 GTCCGTCTCCCTGAGTCTTCTGTATGTCACCCGTCAAGACGTGGGACAGAGAGCTC 975  
 Db 1021 GTCCGTCTCCCTGAGTCTTCTGTATGTCACCCGTCAAGACGTGGGACAGAGAGCTC 1080  
 Qy 976 AAGTCAAGAGTGTGTCTCTCCCGTTACTGTTAGTTAGAGAAATCTCCGGGAAACAAGA 1035  
 Db 1081 AAGTCAAGAGTGTGTCTCTCCCGTTACTGTTAGTTAGAGAAATCTCCGGGAAACAAGA 1140  
 Qy 1036 ATTCACCTTGCTCTTGAAGCGGGGATTGGTAGACATCAAGAGACAACAAGGTTGCGTGG 1095  
 Db 1141 ATTCACCTTGCTCTTGAAGCGGGGATTGGTAGACATCAAGAGACAACAAGGTTGCGTGG 1200  
 Qy 1096 ATTCAGAACAAACCGTGAAGCTGCTGCACCAAGTGCAGAGTGCCTGCGGCTCTCATC 1155  
 Db 1201 ATTCAGAACAAACCGTGAAGCTGCTGCACCAAGTGCAGAGTGCCTGCGGCTCTCATC 1260  
 Qy 1156 TGCCTGGCCCTGCAAGCTGCAAGACGTGTGGGGAGACGCTGCCCTTCAACCAACG 1215  
 Db 1261 TGCCTGGCCCTGCAAGCTGCAAGACGTGTGGGGAGACGCTGCCCTTCAACCAACG 1320  
 Qy 1216 CTCACAGGCTGCAAGCGCTTTGTGTTGATCAGGCTCACCCCTCAAGGAGTGTCCGG 1275  
 Db 1321 CTCACAGGCTGCAAGCGCTTTGTGTTGATCAGGCTCACCCCTCAAGGAGTGTCCGG 1380  
 Qy 1276 CGCTGTCTCAATCTGAGAGAAAGAGTTGTCCTGAAGCGCTTCTGCGGTAGCTGTGAG 1335  
 Db 1381 CGCTGTCTCAATCTGAGAGAAAGAGTTGTCCTGAAGCGCTTCTGCGGTAGCTGTGAG 1440  
 Qy 1336 GGAAGTGTGAATAGAGAGTCAAGTGTGTGATGTGACGACTCATAGTTCACAGACTGGG 1395  
 Db 1441 GGAAGTGTGAATAGAGAGTCAAGTGTGTGATGTGACGACTCATAGTTCACAGACTGGG 1500  
 Qy 1396 GAGTGTGAGCTCCGTCCTGTGTTTCAACATGAACTCTTCCAGACAGGCACTGTGAG 1455  
 Db 1501 GAGTGTGAGCTCCGTCCTGTGTTTCAACATGAACTCTTCCAGACAGGCACTGTGAG 1560  
 Qy 1456 GAGTACTACACCTTCTTCCACTCAAGTCTCAGAGACTTGTGCGGCTTGTACTACGCTG 1515  
 Db 1561 GAGTACTACACCTTCTTCCACTCAAGTCTCAGAGACTTGTGCGGCTTGTACTACGCTG 1620  
 Qy 1516 TTAGAAGGCTGGAATGAGACCAAGCTCTCTGCCCTGTGACGTTGAGAGACAAGAAG 1575  
 Db 1621 TTAGAAGGCTGGAATGAGACCAAGCTCTCTGCCCTGTGACGTTGAGAGACAAGAAG 1680  
 Qy 1576 TTCAATGAGCTTAAACAGGAGGCTTCCATATCCACTCCCTTGGAGAGAACGTTTCTTG 1635  
 Db 1681 TTCAATGAGCTTAAACAGGAGGCTTCCATATCCACTCCCTTGGAGAGAACGTTTCTTG 1740  
 Qy 1636 TTTGGGCTCGTGAAGCAAGAGCTGAAGAGGCACTGAGAGTCTGTGAGGCTGTCCGCT 1695  
 Db 1741 TTTGGGCTCGTGAAGCAAGAGCTGAAGAGGCACTGAGAGTCTGTGAGGCTGTCCGCT 1800  
 Qy 1696 CCCCTGGGGGTGAAGACAGAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAACAGCTAT 1755  
 Db 1801 CCCCTGGGGGTGAAGACAGAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAACAGCTAT 1860  
 Qy 1756 GGCACCAACCCAGAGAGACCTTGAAGAGCTTCCACTTTTTCGAGACTGAAGACAA 1815  
 Db 1861 GGCACCAACCCAGAGAGACCTTGAAGAGCTTCCACTTTTTCGAGACTGAAGACAA 1920  
 Qy 1816 GAGTTTGTGCTTGGCATTAACAGCTTCAAGAGAGTGGCTTCCGATTAACAGAGAC 1875  
 Db 1921 GAGTTTGTGCTTGGCATTAACAGCTTCAAGAGAGTGGCTTCCGATTAACAGAGAC 1980  
 Qy 1876 CTGACCTGTATGACATCTTCTCTGCTCCAGACATGTCCGATTTTGGCGGAAATTCGG 1935

Db 1981 CTGACCTGTATGACATCTTCTCTGCTCCAGACATGTCCGATTTTGGCGGAAATTCGG 2040  
 Qy 1936 GTGATGTCAAGAGGATCTTCCCAAGAGATGAGTCCGCTGAGGATGCTGTGCTCCT 1995  
 Db 2041 GTGATGTCAAGAGGATCTTCCCAAGAGATGAGTCCGCTGAGGATGCTGTGCTCCT 2100  
 Qy 1996 CTATGATGCGGGATTAAGACCTTCAATTAAGAGACGTGGAGATTTTCTGCTCATGCTT 2055  
 Db 2101 CTATGATGCGGGATTAAGACCTTCAATTAAGAGACGTGGAGATTTTCTGCTCATGCTT 2160  
 Qy 2056 GGCACCAACCCAGACCTGCGGAGCTGAGACCTGGGACAGACATCCGACAGAGCGGGCC 2115  
 Db 2161 GGCACCAACCCAGACCTGCGGAGCTGAGACCTGGGACAGACATCCGACAGAGCGGGCC 2220  
 Qy 2116 ATGAAGACCTGTGTGCAAGACTGAGGATCCCACTGCAAGATACAGACCTGATGTTT 2175  
 Db 2221 ATGAAGACCTGTGTGCAAGACTGAGGATCCCACTGCAAGATACAGACCTGATGTTT 2280  
 Qy 2176 AGAATGCAAGATTTAACCCCTGTGTGACAGACCTCTGAGAAATGTCATGAGCCACCT 2235  
 Db 2281 AGAATGCAAGATTTAACCCCTGTGTGACAGACCTCTGAGAAATGTCATGAGCCACCT 2340  
 Qy 2236 AACCTAAGATTCCTCAACTTGGAGAGCACTCACTGAAGAGAGATGTAAGATGGCG 2295  
 Db 2341 AACCTAAGATTCCTCAACTTGGAGAGCACTCACTGAAGAGAGATGTAAGATGGCG 2400  
 Qy 2296 TGTGAAGCTTTAAACACCCAAATGTTTGTGAGTCTTGAAGGCTGGAATGGCTGTGGA 2355  
 Db 2401 TGTGAAGCTTTAAACACCCAAATGTTTGTGAGTCTTGAAGGCTGGAATGGCTGTGGA 2460  
 Qy 2356 TTGACCCATGCTGTTTACTGAAGATCTCCAAATCTTTACAGACTTCCCAAGCTGAAA 2415  
 Db 2461 TTGACCCATGCTGTTTACTGAAGATCTCCAAATCTTTACAGACTTCCCAAGCTGAAA 2520  
 Qy 2416 TCTCTGAGCTGTGGAGAGAAACAGGTGACAGACCAAGGAGTAATGCTTCAAGTATGCC 2475  
 Db 2521 TCTCTGAGCTGTGGAGAGAAACAGGTGACAGACCAAGGAGTAATGCTTCAAGTATGCC 2580  
 Qy 2476 TTGAGAGTCTCCCAAGTCCGCTGACAGAGCTGATCTGGAGAGCTGTGATCAGAGCC 2535  
 Db 2581 TTGAGAGTCTCCCAAGTCCGCTGACAGAGCTGATCTGGAGAGCTGTGATCAGAGCC 2640  
 Qy 2536 ACGGTTGCAAGAGTCTGAGCTCAGCCCTGTGACAGAACCGGAGCTTGAACAACCTGTGC 2595  
 Db 2641 ACGGTTGCAAGAGTCTGAGCTCAGCCCTGTGACAGAACCGGAGCTTGAACAACCTGTGC 2700  
 Qy 2596 CTATCCAAACAACAGCTGGGGAAAGAGGTGTAAATCTACTGTGTGATCCATGAGGCTT 2655  
 Db 2701 CTATCCAAACAACAGCTGGGGAAAGAGGTGTAAATCTACTGTGTGATCCATGAGGCTT 2760  
 Qy 2656 CCCACATGATGTGCAAGAGGCTGATGCTGAATCAGTGCACCTGAGCAAGGCTGAGCTGT 2715  
 Db 2761 CCCACATGATGTGCAAGAGGCTGATGCTGAATCAGTGCACCTGAGCAAGGCTGAGCTGT 2820  
 Qy 2716 GGTTTTCTGCACTTGGGCTTAATGGTAACTCAATGAGCTGACGCACTGAGCCTTAAGCATG 2775  
 Db 2821 GGTTTTCTGCACTTGGGCTTAATGGTAACTCAATGAGCTGACGCACTGAGCCTTAAGCATG 2880  
 Qy 2776 AACCTGTGAAGACAATGAGCTGAGACTTCTGTGAGAGGTCAATGAGAAACAATCTTGT 2835  
 Db 2881 AACCTGTGAAGACAATGAGCTGAGACTTCTGTGAGAGGTCAATGAGAAACAATCTTGT 2940  
 Qy 2836 CATCTCAAGACCTGAGGTTGTAAATGTCACTCAACCCCGGAGTCTGTGAGAGCTGTG 2895  
 Db 2941 CATCTCAAGACCTGAGGTTGTAAATGTCACTCAACCCCGGAGTCTGTGAGAGCTGTG 3000  
 Qy 2896 TCTGTGTGATCTGAGAGACAGACCTTAAGAGCTGTGATCTCAAGCAATGAGCTGTG 2955  
 Db 3001 TCTGTGTGATCTGAGAGACAGACCTTAAGAGCTGTGATCTCAAGCAATGAGCTGTG 3060  
 Qy 2956 GGTGACGTTGGGTTGCTGTGCGCTGTGTGAGAGGACTGAAGCAAAAGAACAGTGTCTGACG 3015

Db	3061	GGTGAACGGTGGGGGTTGGCTGGCACTGGTCGAGGGAACTGAAGACAAAAGAACAGTGTTCCTAGC	3120
Qy	3016	AGACTCCGGGTTGMAAGGCACTGGAGCACTGACTTCCTGATTTGCTGTAGGCACTCTCCTTGACC	3075
Db	3121	AGACTCCGGGTTGMAAGGCACTGGAGCACTGACTTCCTGATTTGCTGTAGGCACTCTCCTTGACC	3180
Qy	3076	CTTTCCTGCAACCGGCATCTGACCACTTAAACCTGTGCAGAAATACTTCAGTCCCAA	3135
Db	3181	CTTTCCTGCAACCGGCATCTGACCACTTAAACCTGTGTGAGAAATACTTCAGTCCCAA	3240
Qy	3136	GGAAATGATGAAGCTGTGTGTGGCCCTTGGCCCTGTGCCACGTCTAACTTAAGATAATTGGG	3195
Db	3241	GGAAATGATGAAGCTGTGTGTGGCCCTTGGCCCTGTGCCACGTCTTAACATTAATTAATTGGG	3300
Qy	3196	CTGTGGAATGGCAGTAACTCCTGTGCAAATAAGAACTGTAGAGAAAGTGCAGCTACTC	3255
Db	3301	CTGTGGAATGGCAGTAACTCCTGTGCAAATAAGAACTGTGTAGAGAAAGTGCAGCTACTC	3360
Qy	3256	AAGCCCCGAGTCGTAAATTGACGGTATGGGCACTCTTTTGATGTAAGATGACCGACAC	3312
Db	3361	AAGCCCCGAGTCGTAAATTGACGGTATGGGCACTCTTTTGATGTAAGATGACCGGTAAC	3417

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RESULT 7
US-10-416-642-3
Sequence 3, Application US/10416642
Publication No. US20040043452A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: ARVIZU, Chandra
TITLE OF INVENTION: EMBRYONIC STEM ASSOCIATED PROTEINS
FILE REFERENCE: PF-0842 PCT
CURRENT APPLICATION NUMBER: US/10/416,642
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: 60/249,407
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 3489
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CBI
US-10-416-642-3

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Query Match	77.7%	Score 3133.6;	DB 17;	Length 3489;
Best Local Similarity	95.2%;	Pred. No. 0;		
Matches 3308;	Conservative	0;	Mismatches 4;	Indels 162;
				Gaps 1.

Qy	1	ATGGAAGAGCAAAATCGCTCACTTTTCAGCTACGGGCTGAAATGGTCTCTATGAG	60
Db	1	ATGGAAGAGCAAAATCGCTCACTTTTCAGCTACGGGCTGAAATGGTCTCTATGAG	60
Qy	61	CTAGCAAGAGAAATTTTCAGACATTCAAGAAATTACTAAAGAAATCTTCAGATCG	120
Db	61	CTAGCAAGAGAAATTTTCAGACATTCAAGAAATTTCTAAAGAAATCTTCAGATCG	120
Qy	121	ACCAATGCTCTAATCCACAGTTTAAATCGGAAGGCCAAGTGAATGTCGGGACATC	180
Db	121	ACCAATGCTCTAATCCACAGTTTAAATCGGAAGGCCAAGTGAATGTCGGGACATC	180
Qy	181	CTTTTGACATGACTAATTAATGAGCATCGCTGGGCTACGTCATTTGACATCTTTGAA	240
Db	181	CTTTTGACATGACTAATTAATGAGCATCGCTGGGCTACGTCATTTGACATCTTTGAA	240
Qy	241	AACATGAACCTGGGAAACCTCTCGGAGAAAGGCAAGGGATGACATGAAA-----	289
Db	241	AACATGAACCTGGGAAACCTCTCGGAGAAAGGCAAGGGATGACATGAAAATTCACAGAA	300
Qy	290	-----	289

Db	301	GATCCTGAAGCAACGATGATCTGACCAAGAACCAACAGCAAGAAAAGTGCAGAAAATAA	360
Oy	290	-----	289
Db	361	TATGGCATGACTAAGCTTATCTTGGGGTGTCGACATCTCGATATATAACAC	420
Oy	280	-----AAATTCAACAGCTATGGAAACAAGAGT	318
Db	421	AAGTATGTTGGAATTCAATTCTTTTGCAGAAATTTCAACAGCTATGGAAACAAGAGT	480
Oy	319	GCCAACAGCAGCAGACAGACAGAAAGAACAGAAATTTCAACAGCTATGGAAACAAGAGTGC	378
Db	481	GCCACAGCAGCAGCAGACAGAAAGAACAAATAATTTCAACAGCTATGGAAACAAGAGTGC	540
Oy	379	ACAGCAGCAGACAGACAGAAAGAACAGAGCATGGAGGTGACATCGGGACTACAGAGTCA	438
Db	541	ACAGCAGCAGACAGACAGAAAGAACAGAGCATGGAGGTGACATCGGGACTACAGAGTCA	600
Oy	439	GTGATGACCAAAATTCGCTGAGAGGAGGATGACGTGCTGATGTTTGAAGACACTGCTGT	498
Db	601	GTGATGACCAAAATTCGCTGAGAGGAGGATGACGTGCTGATGTTTGAAGACACTGCTGT	660
Oy	499	GACTGGCCGGAATATGCAACGTTGGCTGGCTTTTGAATTCAACCGGTGGGGCTTCCGG	558
Db	661	GACTGGCCGGAATATGCAACGTTGGCTGGCTGGCTTTTGAATTCAACCGGTGGGGCTTCCGG	720
Oy	559	CCTGGCACGGTGGTTCCTGCACGGAAAGTCAGGAATTTGGGAAATCGGCTCTAGCCGAAG	618
Db	721	CCTGGCACGGTGGTTCCTGCACGGAAAGTCAGGAATTTGGGAAATCGGCTCTAGCCGAAG	780
Oy	619	ATCGGCTGCTGGGGGCAAGGTGGACTTACACAGGGAAATGTTCTCTGACGCTTCTTC	678
Db	781	ATCGGCTGCTGGGGGCAAGGTGGACTTACACAGGGAAATGTTCTCTGACGCTTCTTC	840
Oy	679	CTCCCGGTTAGAGAGATGCACGCGAAGAGAGAGACAGTGTCAACAGATTCACTCCAAG	738
Db	841	CTCCCGGTTAGAGAGATGCACGCGAAGAGAGAGACAGTGTCAACAGATTCACTCCAAG	900
Oy	739	GAGTGGCCAGACTCCACAGGCTCCGGTGACGGAGATCATGTCCCAACAGAAAGGCTGTGG	798
Db	901	GAGTGGCCAGACTCCACAGGCTCCGGTGACGGAGATCATGTCCCAACAGAAAGGCTGTGG	960
Oy	799	TTCAATCATTTGACGGTTTGATGACCTGAGGACTCTGTCTCAACAATGACACAAGGCTCTGC	858
Db	961	TTCAATCATTTGACGGTTTGATGACCTGAGGACTCTGTCTCAACAATGACACAAGGCTCTGC	1020
Oy	859	AAAGACTGGGCTGAGAGCAGACTCCGTTCAACCTCATACGCAGTCTGCTGAGAGGTC	918
Db	1021	AAAGACTGGGCTGAGAGCAGACTCCGTTCAACCTCATACGCAGTCTGCTGAGAGGTC	1080
Oy	919	CTGCTCCCTGAGTCTCTCTGATGTGACACGTCAGAGCGTGGGACACAGAAAGCTCAAG	978
Db	1081	CTGCTCCCTGAGTCTCTCTGATGTGACACGTCAGAGCGTGGGACACAGAAAGCTCAAG	1140
Oy	979	TCAGAGGTGAGTCTCCCGGTTTACCTGTTAGTGAAGGAATCTCGGGGAAACAAGAAATC	1038
Db	1141	TCAGAGGTGAGTCTCCCGGTTTACCTGTTAGTGAAGGAATCTCGGGGAAACAAGAAATC	1200
Oy	1039	CACCTGCTCTTGAGCGGGGATTTGGTAGCATGAGAACACAAAGGTTGCTGCAATC	1098
Db	1201	CACCTGCTCTTGAGCGGGGATTTGGTAGCATGAGAACACAAAGGTTGCTGCTGCAATC	1260
Oy	1099	ATGAAACAACCTGTGAGCTCTGACACAGTCCAGGTGCCCCGCGTGGGCTCTCATCTGC	1158
Db	1261	ATGAAACAACCTGTGAGCTCTGACACAGTCCAGGTGCCCCGCGTGGGCTCTCATCTGC	1320
Oy	1159	GTGACCTCTGACGTGACAGAGCTGATGGGGGAGAGCGTGCGCCCTTCAACCAACGCTC	1218
Db	1321	GTGACCTCTGACGTGACAGAGCTGATGGGGGAGAGCGTGCGCCCTTCAACCAACGCTC	1380
Oy	1219	ACAGGCTGACGCGCGCTTTTGTGTTTCACTAGCTCACCCCTCGAGGCGTGGTCCGCGC	1278

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 Db 2401 CTAAGATCCCTCAACTTGGAGGACCACTGAAAGAAAGATGTAAAGATGCGCTGT 2460  
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Qy 2259 ACCCATGCTGTATCTGAAAGATCTCCCAATCTTTACAGACTTCCCCAGCTGAAATCT 2418  
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 Db 2641 AGAGTCTCCAGTCCGCGCTGTCAGAACTGATTACTGAGAGACTGTGAGCATACAGCCACG 2700  
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RESULT 8  
 US-10-216-645-1  
 ; Sequence 1, Application US/10216645  
 ; Publication No. US20030125282A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEISS, BERTRAM  
 ; APPLICANT: LESSL, MONIKA

APPLICANT: PETERS-KOTTIG, MICHAEL  
APPLICANT: BECKMANN, GEORG  
TITLE OF INVENTION: HUMAN MATER PROTEINS  
FILE REFERENCE: SCH-1910  
CURRENT APPLICATION NUMBER: US/10/216,645  
CURRENT FILING DATE: 2003-01-21  
PRIOR APPLICATION NUMBER: DE 101 39 874.3 41  
PRIOR FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 3926  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-216-645-1

Query Match 77.7%; Score 3133.6; DB 15; Length 3926;  
Best Local Similarity 95.2%; Pred. No. 0;  
Matches 3308; Conservative 0; Mismatches 4; Indels 162; Gaps 1;

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Db 2401 CTAAGATCCCTCAACTTGGGAG 2460  
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Db 2941 CTTGTGAG 3000

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RESULT 9  
US-10-092-900A-347  
Sequence 347, Application US/10092900A  
Publication No. US2004004382A1  
GENERAL INFORMATION:  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Taupier Jr., Raymond J.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Li, Li  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Gusev, Vladimir Y.  
APPLICANT: Ut, Weizhen  
APPLICANT: Gorman, Linda  
APPLICANT: Miller, Charles E.  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Patturajan, Meera  
APPLICANT: Gangoli, Beba A.M.  
APPLICANT: Verneet, Corine A.M.  
APPLICANT: Guo, Xiaojia Saeha T.  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Fernandes, Bima R.  
APPLICANT: Caeman, Stacie J.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Liu, Yi  
APPLICANT: Anderson, David W.  
APPLICANT: Spaderna, Steven K.  
APPLICANT: Carterton, Elina  
APPLICANT: Leite, Mario W.  
APPLICANT: Zhong, Haihong  
APPLICANT: Alsobrook, John P.  
APPLICANT: Lepley, Denise M.  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Burgess, Catherine B.  
TITLE OR INVENTION: No. US20040043382A1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-290C  
CURRENT APPLICATION NUMBER: US/10/092,900A

CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: USNS 60/274,322  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USNS 60/283,675  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: USNS 60/338,092  
PRIOR FILING DATE: 2001-12-03  
PRIOR APPLICATION NUMBER: USNS 60/274,281  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USNS 60/274,191  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USNS 60/325,681  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: USNS 60/304,354  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: USNS 60/279,995  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: USNS 60/294,899  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: USNS 60/287,424  
PRIOR FILING DATE: 2001-04-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 768  
SEQ ID NO 347  
LENGTH: 3226  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (69)..(3168)  
US-10-092-900A-347

Query Match 71.9%; Score 2900.6; DB 17; Length 3226;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2903; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 406 CATGAGGTGACACATGAGGACCTACAGAGTACGATGATGACCAATTGCTGAGGAGGAG 465  
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QY 466 GATGACGTCTGATGTTTGAACACATGCTGCTGACCTGCGGAAATGCAAACTTTGCT 525  
DB 309 GATGACGTCTGATGTTTGAACACATGCTGCTGACCTGCGGAAATGCAAACTTTGCT 368  
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DB 369 GGTGCTTTTGAATCAGACCGGTGGGCTTCCGGCTCCGACGGTGTCTGACGGAAG 428  
QY 586 TCAGGAATTGGGAATGGGCTTACGCGAAGAGATCGTGTGTGGGCGCAAGGTGA 645  
DB 429 TCAGGAATTGGGAATGGGCTTACGCGAAGAGATCGTGTGTGGGCGCAAGGTGA 488  
QY 646 CTCTACAGGGAATGTTCTCTACGCTCTTCTCCCTCCGTTAAGAGATGCAAGCGAAG 705  
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QY 706 AAGGAGAGCACTGTCAAGAGTTCCTCAGGAGTGGCAAGTCCCAAGCTCCGGTG 765  
DB 549 AAGGAGAGCACTGTCAAGAGTTCCTCAGGAGTGGCAAGTCCCAAGCTCCGGTG 608  
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DB 609 ACGGAGATCATGTCCCGACGAAAGGCTGTGTTCATCATTTGACGGTTGATGAGCTG 668  
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QY 946 ACCGTGAGAGCGTGGGACAGAGAAAGTCAAGTCAAGTCTGCTCCCGTTACTG 1005

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DB 969 TGCAGGTGCGCGGTGGGCTTCTCATCTGCGTGGCTTGCAGCTGACAGACGTGTG 1028  
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QY 1246 CATGAGCTCACCCCTCGAGGGGTGGTCCGGGCTGTCAATCTGAGAGAAAGATTGTC 1305  
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DB 1269 AACATCTCTTCCAGACAGCACGTTGAGAGATCTACCTTCTCACCTCAGTCTC 1328  
QY 1486 CAGGACTTCTGTGCGGCTTGTACTACGTTTGAAGGCGCTGGAATGAGCAGCTCTC 1545  
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DB 1509 CCACTGAGGTCTGTGGGCTGTCCGTTCCCTGGGGGTGAAGCAGAACTTCTGAC 1568  
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DB 1629 TTCCATCTCTTTTGAAGCTCAAGACAAAGATTTGTGGCTTGGCAATTAAACGCTTC 1688  
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QY 1906 CAGCATGTCCGTATTTGGGAAATTCGGGTGATGATCAAAAGGATTTCTCCAAAGAT 1965  
DB 1749 CAGCATGTCCGTATTTGGGAAATTCGGGTGATGATCAAAAGGATTTCTCCAAAGAT 1808  
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DB 1809 GAGTCCGTGAGGAGATGCTGTGTCCCTTATGAGTGGGGAATTAAGACCTCATAGG 1868  
QY 2026 GAGCATGAGAAAGATTTCTGCTCATGCTTGGCAACCACTGCGGCACTGAGC 2085



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Qy 2206 CACCTGTGGAATTCATGCGGCAACCGTAACCTGAATCCCTCAATTGGGAGGACCC 2265  
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Db 2109 CACCTGTGGAAGAGAGATGTAAGATGCGGTGAGAGCTTTAAACCCAAATGTTTG 2168  
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Qy 2686 AATCAGTGCACCTGAGACAGGCTGGCTGTGGTTTCTTTCGACCTTGGCTTAAGGATAC 2745  
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Qy 2746 TCATGCTGAGAGAGCACTGAGCCTTAGAGATGAACCTGTGAGAAACAATGGGTGAAGCTT 2805  
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Qy 2926 AAGAGCTGTGATCTCAAGAGAACATGCTGTGGTGAAGGAGTGTGCTGTGCGAG 2985  
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Qy 2986 GGAAGTGAAGAAAGAAAGATGTTCTGAGAGACTGCGGTTTGAAGGAGATGAGACTGACT 3045  
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Qy 3106 AACCTGTGTGAGAAATTAATTAATGATCCCAAGAGATGATGAAGCTGTGTTGGCCTTTGGC 3165  
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Qy 3166 TGTCCACGCTTAACCTTAAGATTAATTGGCTGTGAAATGGCAGTACCTGTGCAATA 3225  
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Qy 3226 AGAAGAGCTGTGAGAGAAAGTGCAGACTACTCAAGCCCGGAGTGTGAAATGAGAGTGTG 3285  
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Qy 3286 CATCTTTGATGAGAGATGAGCCGACAC 3312  
Db 3129 CATCTTTGATGAGAGATGAGCCGCTAC 3155

RESULT 10  
US-10-399-443-5  
; Sequence 5, Application US/10399443  
; Publication No. US2004002869A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute  
; APPLICANT: Health  
; APPLICANT: Nelson, Lawrence M.  
; APPLICANT: Tong, Zhi-Bin  
; APPLICANT: Nelson, Lawrence  
; APPLICANT: Zhi-Bin, Tong  
; TITLE OF INVENTION: Human Gene Critical to Fertility  
; FILE REFERENCE: 4239-64785  
; CURRENT APPLICATION NUMBER: US/10/399,443  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/241,510  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: PCT/US01/10981  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 3447  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-399-443-5

Query Match 31.7%; Score 1278; DB 17; Length 3447;  
Best Local Similarity 67.2%; Pred. No. 0;  
Matches 1898; Conservative 0; Mismatches 908; Indels 18; Gaps 6;

Qy 498 TGAATGCGCCGGAATGGAACGTTGGCTGTGATCTTGAATTCACACCGGTGGGCTCCG 557  
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Qy 558 GCTTCGACAGGATGTTCTGACAGGAAAGTCAAGAAATGGGAAATCGGCTTACCCAGAG 617  
Db 575 GCTTCACACATTAATCTTACATGAGAACAGAGAGTGGAGAGTGTGGCCAGAG 634  
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Db 635 TATGTTCTTGGCTGGGCAAGGTTAACTTTCACAAATAATG---TCTTTGTCACTCTT 691  
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Db 752 GGAATGGCGAGACTCCGATGATGATGACAAAGATCATGATCCGACCAAGAAAGAGTGT 811  
Qy 798 GTTCATATGACCGATTCATGATGACCTGTGCTGTCTC---AACATGACAAAGCT 854  
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Qy 855 CTGCAAGAGCTGGCTGAGAGAGAGCTCCGTTCAACCTCATACGCAAGTGTGCTGAGAGAA 914  
Db 872 ATCCAGAGACTGGAAGATGAAAGCCCATATATCATCTGATGTATACAGCTCTGAGAGAA 931



Qy	915	GGTCCTGCTCCCTGAGTGCCTTCTCTATGCTGACCGCTGAGAGCGTGGGACAGAGAGGT	974
Db	932	GGCTCTTCACTCAAGTCTCTTCTCATCTATTACACAGAAACAAGGCTTAGAAAACT	991
Qy	975	CAAGTCAGAGGTCGTGTCTCCCGTTACCTGTTAGTAGGGAATCTCGGGGAAACAAAG	1033
Db	992	CAAGTCATGAGTGTGTGTCGCCCTCTATATATCTGGTTGAAGGACTGTCTGCATCAAGGAG	1053
Qy	1035	AATCCACTTGGCTCTTGAGCCGGGGAATTGGTAGGATCAAGAAACAAGAGGTGCGTGC	1099
Db	1052	ATCTCAGCTGGTCTCGAAGAACATCTCCAAATAGCTGTATGAATACAAATCTTCCATTTC	1111
Qy	1155	CTGCGTGGCCCTGACGCTGACAGAGAGTGTGGGGAGAGCGTGGCCCTTCAACCAAC	1211
Db	1172	CTGTAGGCTCTACAGCTACAGAAAMAACTGGGAAAGAGATGACCCCTACCTGCGACAGC	1233
Qy	1215	GCTCACAAGGCTGACGCGCGCTTGTGTGTTTATCAGCTCACAACCTCGAGCGTGGTCCG	1277
Db	1232	TCTCACCAGGTTGTATGCGCAGGTGGTGTTCACAGCTCACACTTGAAAGGCCCTTCCCA	1299
Qy	1275	GCGCTGTCTCATCTGAGAGAAAGATTGTCTTGAAAGCGCTTCTGCGGTAGGCTGTGGA	1333
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Qy	1395	GAAGCTGAGCTCCGTCGCTGTGTTTCACATGAAACATCCCTCTCCGACAGAGCC--ACTG	1451
Db	1412	GGAGCTGAGATCTTGGCCCTCTTTCATATGAACATCTCTTCCAGGTTGGCACAACAG	1477
Qy	1452	TGAGAGTACTACACCTTCTTTCACCTCACTTCCAGACTTGTGCGCGCTTGACTA	1511
Db	1472	TGAGCAGTGTATATGTTTCTCCCACTCAGCTGAGAGATTTCTTGTGCTGTATATTA	1533
Qy	1512	CGTGTTAAGGGCCCTGGAATGAGCCAGCTCTGCGCCCTGTAGCGTTGAGAAACAACAA	1577
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Db	1706	CGTATTTCCACTGTGTAGGAGAACTCCAAACACTGGGCTCTCTGATAGCTCACAAGT	1765
Qy	1752	TAAATCCACACCCAGAGAGACCTCTGAGCGCTTCCACTGTCTTTTGAAGCTCAAGA	1811
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Qy	1812	CAAGAGTTTGTGCTTGGAATTAAACAGCTTCCAAAGAGTGGGCTTCGATTAACA	1877
Db	1826	TGAGAGTTTGTGGCGGGGCTCTCAAAACGCTTCCAAAGAGTGGGCTGCTGATTAACA	1888
Qy	1872	GAACTGGACTTATAGCATCTTCTCTTGTGCTCTCAGCACTGTCCGTATTTGCGGAAAT	1933
Db	1886	GAAATGAGACTTGAAGGTCTTCTCTACTGTCTCAAGCACTGTCAAGAACTTGAAGCAAT	1945
Qy	1932	TGCGGTGATGTCAAGAGGATTTTCCCAAGAGATAGATTCGCTGAGGCAATGTCTGTGT	1999
Db	1946	CCGGGTGATATCAAGAGACTCTCTCTGGTATATATATCTCTCGAGCTGTGCGCTGTGT	2005

QY	1992	CCCTCTAATGATGGGGG- - - TAAGACCTCATTTGAGAGAGGAGGAAATTTCTCTC	2048
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QY	2049	CATCTTGGCACCACCCACACCTGCGGAGCTGGA CCTGGGAGACATCTTGACAGA	2108
Db	2066	TGTGCTTGAGCCTCCGGAACTTGAAAGAGCTGGA CTTGGGGACACAGCATCTGAGTCA	2125
QY	2109	GGGGGCCATGAAACCTGTGTGCGCAGCTGAGGCATCCACCTGCAAGATACGACCT	2168
Db	2126	ACGGGCCATGAAAGTACTGTGCTCCGAGCTGCGGAATCAGTCTGCGAATAACGAAGCT	2185
QY	2169	GATGTTTAAAGAAATGACAGATTAACCCCGGTGTGACAGACCTCTGGAAGATCGATGCG	2228
Db	2186	GACGTTTAAAGTACAGAGTGAAGTGTGTCTGGCTTAAACATCTCTGAAAGCTCTTTTAA	2245
QY	2229	CAACCTGAACCTTAAGATCCCTCAACTTGGAGGAGCACCACCTGAAGAGAGATGTAA	2288
Db	2246	CAATCAAAACCTTAAGTACTCATCTGAAGGAAACCTCCATGAAGATGATGACATGAA	2305
QY	2289	GATGGCGGTGAGACCTTTAAACACCCAAAATGTTTGTGAGTCTTTAGGCTGGAATG	2348
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QY	2349	CTGTGAGATGAGCCCATGCTGTTTACTCGAAGATCTCCCAAATCCTTAAGACCTCCCA	2408
Db	2366	CTGTGAGATTAACCATCAATGTGTTTAAAGATGATCTCAACGCTTTATTTCAACACAC	2425
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QY	2469	TGATGCTTGAAGTCTCCAGTGGCCCTGCGAGAGCTGATATCTGAGGACTGTGTCAT	2528
Db	2486	GAATGCTCTGATGATGCTCAATGTGTCTACTGCAAAAGTTGATATCTGACAACTGTGCT	2545
QY	2539	CACGAGCAAGGATGTCGAGAGTCTGCGCTCAGCCTGTGACGAAACCGGAGCTTGAACA	2588
Db	2546	CACACTGCGCAGCTGCCACCTTCTGATCTCAGGCCCTTTTACGCAACCAAGACTTGAACA	2605
QY	2589	CCGTGCTCTAATCCAAACAAGCCTGGGGGAAAGAAAGTGTAAATTTACTGTGTGATCAT	2648
Db	2606	CTGTGCTCTGTCAAAACAAGCCTGGGGA CTGAAGAGTGCACAGCTGTGTCAGTTCT	2665
QY	2649	GAGGCTTCCCACTGTAGTCTGCGAGAGCTGATGCTGAATCAAGTGCACCTGACACGGC	2708
Db	2666	GAGGAATCCAGAAATGTGCTCTCGAGGGCTGTATCTGAATCACTGCAACATGTAAATGA	2725
QY	2709	TGCGTGTGTGTTTCTTGACACTTGCGCTTTAATGGGTAATCAATAGCTGACGACTGAGCT	2768
Db	2726	TGCTTAAATGTGCTCTGCGCAATGAGACTTTGCAACCAACAAGCTGACCACTGAGACT	2785
QY	2769	TAGCATTAACCTGTGGAAGCAATGGCGTGAAGCTTGTGCGGAGGTCAATGAGAGAAC	2828
Db	2786	GACCATTAACCCGTAAGGAGTGTGGAATGAGACTGTGTGTAAGCTTTAAAGAAAC	2845
QY	2829	ATCTTGTCAATCTCAGAGACTGAGAGTGTAAAGTGCATCTCAACCGCGGTGCTGTGA	2888
Db	2846	TACTTGTTAACCTCAABAACCTGAACTAAGTGAATGCACTCAACAGAACTGTGCGA	2905
QY	2889	GAGTCTGTCTGTGTGATCTTGAGAGACAGACACTGAAGAGCCTGATCTCACGGAACA	2948
Db	2906	GGAACCTGAGCTGTATGATCAACAACAACAGCACTTAAAAAGTTTGATCTTGGTAAACA	2965
QY	2949	TGCGCTGGGTGACGATGGGTGTGCTGGCGTGTGAGAGGACTGAAGCAAAAGAACATGT	3008
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QY	3009	TCTGACAGAGACTCGGATGTGAAGGACTGTGACATCTTGATTTGCTGTAGGCACTCTC	3068
Db	3026	CTGTAGAGAGACTTGGGTGGGGGCAATTAAGTTGACTTCCAAATTTGCTGTAGGCAATTTCT	3085
QY	3069	CTTGGCCCTTTCTGCAACCGGCACTGACACAGCTTAAACCTGGGTGCAAAATTAATTCA	3128

Accession	Sequence	Position
Db	ATTGGCCATCTTGGCAACCTCCACTGAACAGCTTAACCTGGTAAGAAATGACTTCAG	3145
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Qy	3189 AATTGGGCTGTGGAATAATGGCAGTACCTGTGCGAATAATGAAGAAGCTGTGAGAGAAATGCA	3248
Db	3206 AATTGGCTGTGGAAGCAGCAGAGTACTATAGCCGAGGTGAAGAAAGACAGCTGGAGGAATTGA	3265
Qy	3249 GCTACTCAAGCCCGCAGTCGTAACTATGACAGGATGGCATCTTTTATGTAAGAAATGACCG	3308
Db	3266 GTTGTCAAGCCCGCAGCTGTGATTTGAATGGTGATTTGGTATGCTAGTGAATGAAGATGACCG	3323
Qy	3309 ACAC 3312	
Db	3326 AAAC 3329	

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RESULT 11
US-10-677-943-5
; Sequence 5, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
APPLICANT: The Government of the United States of America as
APPLICANT: represented by the Secretary of the Department of Health and
APPLICANT: Human Services
APPLICANT: Nelson, Lawrence
APPLICANT: Tong, Zhi-Bin
TITLE OF INVENTION: Human Gene Critical to Fertility
FILE REFERENCE: 4239-64790
CURRENT APPLICATION NUMBER: US/10/677,943
CURRENT FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: 60/241,510
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: PCT/US02/05776
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/US01/10981
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
; LENGTH: 3447
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-677-943-5

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Query Match	31.7%	Score 1278;	DB 17;	Length 3447;
Best Local Similarity	67.2%;	Pred. No. 0;		
Matches 1898;	Conservative	0;	Mismatches 908;	Indels 18; Gaps 6;
QY	498	TGACTGGCGGAAATGC	CGTGGCTTTTCA	TTCAGACGGGTGGGCTTCG 557
Db	515	TGACAGCCAGATGAAT	TATTTCTGATGCTTTT	TAACCATTCAGAAACCTTCCA 574
QY	558	GCCTCGCAGGTGTTCT	GACGGAATGCAGATTGG	GAATCGCTTCAGCAGAG 617
Db	575	GCTTCACACATTAAT	CTCAATGGAAGACAGAA	GTGGAAAGTACGTTTGGCCAGAG 634
QY	618	GATCGTGTGTGTGGG	CGCAAGTGACTCTA	CCAGGAAATGTTCTCTACGTTCTT 677
Db	635	TATGTGTTCTTGAGT	GGGCGACAGGGTAAC	TCTCCAAAAATG---TCTTTGTCATCTT 691
QY	678	CCTCCCCCTTAGAGAT	GCAGCGGAAGAAAGAG	CGATGTCACAGAGTTCAATCCAG 737
Db	692	CTTCTCTGTTAGAATA	TAAGTGGACAGAAAGCA	GTTTGGCAGCGCTGATTTGCATA 751
QY	738	GGAAGGGCAGACCTCC	AGGCTCCGGTACCGGA	AGATCATGTCCGACAGAAAGGCTTT 797
Db	752	GGAAGTTCACAGCTCT	CTGGAGATCTAATGTA	CAAAAGTCATATGTCCCAACAGAAAGACTTT 811
QY	798	GTTTCATCTTAGACGG	TTTCGATGACTTGGGCT	CTGTCTC---AACATGACAGAAAGCT 854

Db	81.2	GTTTGTCAATGATGCGCTTGGATGATGATGAGACTGTCTCTCCAACTGATGATGATGACACT	871
Qy	855	CTGCAAAAGCTGCGGCTGAGAGACAGCCCTCCGTTCAACCTCATAGCAGATCTGTGAGGAA	914
Db	872	ATCCAGAACTGGAAGATGAAACAGCCCATATACATCTGTATGTACAGCCTCTGAGGAA	931
Qy	915	GGTCTGTGCTCCCTGAGTCCTTTCGTATGTCACCGTCAAGACGTGGGCAAGAAAGCT	974
Db	932	GGCTCTTACCTCAGTCTCTTCTCATATACCAACAGAAACACAGGCTTAGAAAAACT	991
Qy	975	CAAGTCAGAGGTCCGTGTCTCCCGTTACTGTATGATGAGAAATCTCCGGGAAACAAAG	1034
Db	992	CAGTCGAATGTTGTGTCTCCCTCTATATCTGGTTGAAAGACATCTGTGATCAAGAG	1051
Qy	1035	AATTCAGTTCCTCCCTTGAAGCGCGGGAATGTGAGACATCAGAAAGACAAGGGTTCGTC	1094
Db	1052	ATCTCAGCTGGTCTCTCGAAGAACTCCAAATGATGTATGAAATCAAGCTTTCATTC	1111
Qy	1095	GATCATGAACAACCGGTGAGTCTCTGCACAGTGCAGAGTGC CGCGGTGAGCTCTCAT	1154
Db	1112	TCTGATAGAAATCAACGAGCTGTTTGAACCAATGCGACGCCCCCTGTGTGTCTCCCTGT	1171
Qy	1155	CTGCGTGGCCCTGACAGCTGCAGAGAGTGTGGGGGAGAGCGTCCGCCCTTCACCAAC	1214
Db	1172	CTGTAGGCTCTACAGCTACAGAAAGAACTGGGAAAGATGCAACCTTACCTGCACAC	1231
Qy	1215	GCTCACAGGCGTGCACGCGCGCTTTTGTATTCATCAGTCTCAACCCCTGAGGCGTGTCCG	1274
Db	1232	TCTCACCGGTTTGTATGTCCAGCTGTGTGTTCACCAAGTCTCACTTGAAAGGCTTCCCA	1291
Qy	1275	GCGCTGTCTCAATCTGAGAGAAAGATGTCTGAGAGCGCTTTCGCGTATGCTGTGA	1334
Db	1292	GAGCGCTCTCAGTCAAGAAAGACAGATTACTGTAGTGGATTGTGATGATGCGAGCTGA	1351
Qy	1335	GGAAGTGTGGAATGAGAACTCAGTGTTTGATGTGTGACACACTCATGTTCAAGACTCGG	1394
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Qy	1395	GGAGCTGAGGCTCGGTCTGTGTTTCAATGAACATCCTTCCCAAGACACCC---ACTG	1451
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Qy	1452	TGAGGAGTACTACACTTCTTCCACTTCAGTCTCCAGGACTTGTGCGCGCTGTACTA	1511
Db	1472	TGAGCAGTGTATATGTTTCTTCCCACTCAGCGTGAAGATTCTTGTGTGCTTATATTA	1531
Qy	1512	CGTGTGAGGCGCTGAAATCGACCAAGCTCTGCTCTGTATCGTTGAGAAACAA	1571
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Qy	1572	GAGGTCCATGAGCTTAAACAGGCGCTTCATATCCACTCGCTTGGAGAAAGCGTTT	1631
Db	1589	GAGCATCAATGAGGTGAAGAGAACTGACAGACATGCGCTC---CTCGGAATGAAGCGTTT	1645
Qy	1632	CTTGTGTGGCCTCGTGAAGCGGAAGACGTATGAGAGGCACTGAGAGTCTGCTGCGCTGTCC	1691
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Qy	1692	CGTTCCCTGCGGCTGAAGCAGAACTTCTGCACTGGTCTCTGTGTGGTCAAGACC	1751
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Qy	1812	CAAAAGATTGTGCTTGCGATTAAACAGCTTCCAAAGATGTGTGCTTCGATTTAACCA	1871
Db	1826	TGAAGATTTTGTGGCGGGGCTCTCAACGCTTCCAAAGATGTGTGGCTGTGATTTAACCA	1885
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QY 1054 CCGGGGATGGTGAGCATCAGAAACAACAAGGTTGGTGAGATCAATGAAACAACCTGAG 1113  
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QY 1114 CTGCTCAGACAGTCCAGAGTCCCGCGTGGGCTCTCATCTGCGAGCCCTGCACTG 1173  
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QY 1174 CAGGACGTGGGGGAGAGCGTCCGCCCTTCAACCAACGCTCAACAGGCTCAGCC 1233  
Db 421 CAGGACGTGGGGGAGAGCGTCCGCCCTTCAACCAACGCTCAACAGGCTCAGCC 480  
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QY 1294 GAAAGAGTTGCTCTGAGACGCTTCTGCGGTATGGCTGAGGAGAGTGTGAATAGGAAG 1353  
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Db 781 GAGCGAGCTCTCTGCGCTCTGTACGTTGAGAAACAAGAGTCCATGAGCTTTAAACAG 840  
QY 1594 GCAGGCTTCCATATCCATCTGCTTGTGATGAAAGGTTTCTGTTGGCTCTGTGAGGAA 1653  
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QY 1654 GACGTAAAGAGGACCACTGAGAGTCTGCTGAGGCTGCTCCGCTTCCCTGAGGGGTAAAGAG 1713  
Db 901 GACGTAAAGAGGACCACTGAGAGTCTGCTGAGGCTGCTCCGCTTCCCTGAGGGGTAAAGAG 960  
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Db 1081 TTAAACAGCTTCAAGAGATGGCTTCCGATTAACCAAGACCTGAGCTTGATAGCATCT 1140  
QY 1894 TCCTTTCGCTCCAGC 1909  
Db 1141 TCCTTTCGCTCCAGC 1156

RESULT 13  
US-10-677-943-1

; Sequence 1, Application US/10677943  
; Publication No. US20040072297A1

; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America as  
; APPLICANT: represented by the Secretary of the Department of Health and

; APPLICANT: Human Services  
; APPLICANT: Nelson, Lawrence  
; APPLICANT: Tong, Zhi-Bin  
; TITLE OF INVENTION: Human Gene Critical to Fertility  
; FILE REFERENCE: 4239-64790  
; CURRENT APPLICATION NUMBER: US/10/677,943  
; PRIOR APPLICATION NUMBER: 2003-10-01  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: PCT/US02/09776  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: PCT/US01/10981  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 1  
; LENGTH: 1157  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-677-943-1

Query Match 28.6%; Score 1152.8; DB 17; Length 1157;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 754 CAGGCTCCGGTGAACGAGATCATGTCCGACCAAGAAAGCTGTGTTCAATCATTCACGGT 813  
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QY 814 TTGCATGACCTGGGCTCTGTCTTCAACAAATGACCAAAAGCTTCGAAAGACTGGGCTGAG 873  
Db 61 TTGCATGACCTGGGCTCTGTCTTCAACAAATGACCAAAAGCTTCGAAAGACTGGGCTGAG 120  
QY 874 AAGGAGCTCCGTTCAACCTCATACGAGTCTGCTGAGAAAGTCTGCTCCAGAGTCC 933  
Db 121 AAGGAGCTCCGTTCAACCTCATACGAGTCTGCTGAGAAAGTCTGCTCCAGAGTCC 180  
QY 934 TTCTGATCTGACCGTCAAGAGAGTGGGCAACAGAAAGCTCAAGTCAAGAGTCTGTCT 993  
Db 181 TTCTGATCTGACCGTCAAGAGAGTGGGCAACAGAAAGCTCAAGTCAAGAGTCTGTCT 240  
QY 994 CCCCCTTACCTGTTAGTTAGAGAAATCTCCGGGGAACAAAGAAATCCATTGCTCTTGAG 1053  
Db 241 CCCCCTTACCTGTTAGTTAGAGAAATCTCCGGGGAACAAAGAAATCCATTGCTCTTGAG 300  
QY 1054 CCGGGGATGGTGAGCATCAGAAACAACAAGGTTGGTGAGATCAATGAAACAACCTGAG 1113  
Db 301 CCGGGGATGGTGAGCATCAGAAACAACAAGGTTGGTGAGATCAATGAAACAACCTGAG 360  
QY 1114 CTGCTCAGACAGTCCAGAGTCCCGCGTGGGCTCTCATCTGCGAGCCCTGCACTG 1173  
Db 361 CTGCTCAGACAGTCCAGAGTCCCGCGTGGGCTCTCATCTGCGAGCCCTGCACTG 420  
QY 1174 CAGGACGTGGGGGAGAGCGTGGCCCTTCAACCAACGCTCAACAGGCTGCAAGCC 1233  
Db 421 CAGGACGTGGGGGAGAGCGTGGCCCTTCAACCAACGCTCAACAGGCTGCAAGCC 480  
QY 1234 GCTTTTGTTTCAATCAAGCTCAACCCCTGAGGCGTGGTCCGCGCTGCTCAATCTGAG 1293  
Db 481 GCTTTTGTTTCAATCAAGCTCAACCCCTGAGGCGTGGTCCGCGCTGCTCAATCTGAG 540  
QY 1294 GAAAGAGTTGCTCTGAGACGCTTCTGCGGTATGGCTGAGGAGAGTGTGAATAGGAAG 1353  
Db 541 GAAAGAGTTGCTCTGAGACGCTTCTGCGGTATGGCTGAGGAGAGTGTGAATAGGAAG 600  
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Db 601 TCAGTGTGTTGATGGTGAACGCTCATGGTTCAAGGACTCGGGAGTCTGAGCTCCGTGCT 660  
QY 1414 CTGTTTCAATGAACATCTCTTCTCCCAAGACGCACTGTGAGAGTACTACCTTCTTC 1473  
Db 661 CTGTTTCAATGAACATCTCTTCTCCCAAGACGCACTGTGAGAGTACTACCTTCTTC 720

QY 1474 CACCTGAGTCTCCAGAGCTTCTGTGCGGCTTTGTAAGTGTGAGAGGCGCTGGAATC 1533  
DB 721 CACCTGAGTCTCCAGAGCTTCTGTGCGGCTTTGTAAGTGTGAGAGGCGCTGGAATC 780  
QY 1534 GAGCAGCTCTCTGCGCTCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1593  
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QY 1594 GCAGGCTCTCCATATCCATCTGCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1653  
DB 841 GCAGGCTCTCCATATCCATCTGCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 1654 GAGCTGAG 1713  
DB 901 GAGCTGAG 960  
QY 1714 AGCTTCTGAGCTGAGTCTCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1773  
DB 961 AGCTTCTGAGCTGAGTCTCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020  
QY 1774 ACCCTGAG 1833  
DB 1021 ACCCTGAG 1080  
QY 1834 TTAAACAGCTTCCAGAGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1893  
DB 1081 TTAAACAGCTTCCAGAGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
QY 1894 TCCTTCTGCTCCAGC 1909  
DB 1141 TCCTTCTGCTCCAGC 1156

## RESULT 14

US-10-399-443-3  
; Sequence 3, Application US/10399443  
; Publication No. US20040028669A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute  
; APPLICANT: Health  
; APPLICANT: Nelson, Lawrence M.  
; APPLICANT: Tong, Zhi-Bin  
; APPLICANT: Nelson, Lawrence  
; APPLICANT: Zhi-Bin, Tong  
; TITLE OF INVENTION: Human Gene Critical to Fertility  
; FILE REFERENCE: 4239-64785  
; CURRENT APPLICATION NUMBER: US/10/399,443  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/241,510  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: PCT/US01/10981  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1075  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-399-443-3

Query March 18.8%; Score 756.6; DB 17; Length 1075;  
Best Local Similarity 99.5%; Pred. No. 1.3e-215;  
Matches 759; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2550 TCTGAGCTCAGAGCTCTGTCAGCAACCGAGCTTGAACAGCTGTGCTTATCAACAG 2609  
DB 1 TCTGAGCTCAGAGCTCTGTCAGCAACCGAGCTTGAACAGCTGTGCTTATCAACAG 60  
QY 2610 CTTGGGAG 2669  
DB 61 CTTGGGAG 120

QY 2670 GCAGAGAGCTGATGCTGAATCAGTGTGACCTGAGACAGGCTGTGCTGTTCTTGCACT 2729  
DB 121 GCAGAGAGCTGATGCTGAATCAGTGTGACCTGAGACAGGCTGTGCTGTTCTTGCACT 180  
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DB 181 TCGCTTATGGGTAACTCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
QY 2790 CAATGAGCTGAGAGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2849  
DB 241 CAATGAGCTGAGAGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
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DB 301 GAGAGTGTAAAGTGTATCTACCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
QY 2910 GAG 2969  
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QY 3210 GTACCTGTGCAATTAAG 3269  
DB 661 GTACCTGTGCAATTAAG 720  
QY 3270 AATTGACGTTAGTGTGATCTTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3312  
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US-10-677-943-3  
; Sequence 3, Application US/10677943  
; Publication No. US20040072297A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America as  
; APPLICANT: represented by the Secretary of the Department of Health and  
; APPLICANT: Human Services  
; APPLICANT: Nelson, Lawrence  
; APPLICANT: Tong, Zhi-Bin  
; TITLE OF INVENTION: Human Gene Critical to Fertility  
; FILE REFERENCE: 4239-64790  
; CURRENT APPLICATION NUMBER: US/10/677,943  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: 60/241,510  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: PCT/US02/09776  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: PCT/US01/10981  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 1075  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-677-943-3

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Query Match      18.8%; Score 756.6; DB 17; Length 1075;
Best Local Similarity 99.5%; Pred. No. 1.3e-215;
Matches 759; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2550 TCTGGCCCTCAGCCCTCCGACGACACCGAGCTTGACACCTGTGCCCATTCCACCAACAG 2609
DB 1 TCTGGCCCTCAGCCCTCCGACGACACCGAGCTTGACACCTGTGCCCATTCCACCAACAG 60
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Database :

Published Applications NA:\*

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21:	/cgnt2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22:	/cgnt2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
1	1344	100.0	4035	14	US-10-124-498-5	Sequence 5, Appli
2	1344	100.0	4035	14	US-10-066-521-5	Sequence 5, Appli
3	1006	74.9	3489	17	US-10-416-642-3	Sequence 3, Appli
4	1006	74.9	3926	15	US-10-216-645-1	Sequence 3, Appli
5	988	73.5	3830	15	US-10-216-645-3	Sequence 3, Appli
6	968	72.0	3226	17	US-10-092-900A-347	Sequence 347, App
7	616	45.8	3885	18	US-10-860-761-3	Sequence 3, Appli
8	616	45.8	3900	17	US-10-399-443-23	Sequence 2, Appli
9	616	45.8	3900	17	US-10-677-943-23	Sequence 2, Appli
10	385	28.6	1157	17	US-10-399-443-1	Sequence 1, Appli
11	385	28.6	1157	17	US-10-677-943-1	Sequence 1, Appli
12	196	14.6	1075	17	US-10-399-443-3	Sequence 3, Appli
13	196	14.6	1075	17	US-10-677-943-3	Sequence 3, Appli
14	57	4.2	2099	13	US-10-027-632-258159	Sequence 28159,
15	57	4.2	2099	17	US-10-027-632-258159	Sequence 28159,
16	12	0.9	509	16	US-10-029-386-10957	Sequence 10957, A
17	12	0.9	1704	16	US-10-029-386-24660	Sequence 24660, A
18	12	0.9	3108	10	US-09-965-621-23	Sequence 23, Appli
19	12	0.9	3108	17	US-10-407-866-23	Sequence 22, Appli
20	12	0.9	3108	18	US-10-781-294-23	Sequence 17, Appli
21	12	0.9	3186	14	US-10-124-498-17	Sequence 17, Appli
22	12	0.9	3186	14	US-10-066-521-17	Sequence 67, Appli
23	12	0.9	3218	17	US-10-407-866-67	Sequence 5, Appli
24	12	0.9	3447	17	US-10-399-443-5	Sequence 5, Appli
25	12	0.9	3447	17	US-10-677-943-5	Sequence 5, Appli
26	12	0.9	3466	17	US-10-108-260A-718	Sequence 718, App
27	12	0.9	4931	15	US-10-028-374-1	Sequence 1, Appli
28	12	0.9	4931	16	US-10-183-770-1	Sequence 1, Appli
29	10	0.7	610	17	US-10-424-599-139217	Sequence 139217,
30	9	0.7	240	16	US-10-029-386-16506	Sequence 16506, A
31	9	0.7	270	11	US-09-922-293-1943	Sequence 1943, Ap
32	9	0.7	339	18	US-10-437-963-16943	Sequence 46914, A
33	9	0.7	346	18	US-10-425-115-150063	Sequence 150063,
34	9	0.7	394	18	US-10-425-115-72548	Sequence 72548, A
35	9	0.7	426	18	US-10-674-124A-25173	Sequence 25173, A
36	9	0.7	438	18	US-10-357-930-38072	Sequence 38072, A
37	9	0.7	440	17	US-10-424-599-35497	Sequence 35497, A
38	9	0.7	564	16	US-10-029-386-2806	Sequence 2806, Ap
39	9	0.7	578	10	US-09-764-891-1745	Sequence 1745, Ap
40	9	0.7	693	18	US-10-363-345A-27001	Sequence 27001, A
41	9	0.7	693	18	US-10-363-345A-27115	Sequence 27115, A
42	9	0.7	693	18	US-10-363-345A-27116	Sequence 27116, A
43	9	0.7	720	13	US-10-027-632-150437	Sequence 150437,
44	9	0.7	720	13	US-10-027-632-150437	Sequence 150437,
45	9	0.7	720	17	US-10-027-632-150437	Sequence 150437,

## ALIGNMENTS

RESULT 1  
US-10-124-498-5  
; Sequence 5, Application US/10124498  
; Publication No. US20030017983A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Wang, Weiye  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
; FILE REFERENCE: 07334-367001  
; CURRENT FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US/10/124,498  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/318,645  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/265,231  
; PRIOR FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 25



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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4032)
US-10-124-498-5

Alignment Scores:
Pred. No.: 0 Length: 4035
Score: 1344.00 Matches: 1344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

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Db 1 ATGAGAGAGACAATATGCTCACCTTTCCAGCTACGGGCTGCAATGGTGTCTATAGAG 60
Qy 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysSerSerGluSer 40
Db 61 CTAGACAGAGAAAGATTTCAGACATTCAAGAAATTACTAAAGAAATCTTCAGAAATCG 120
Qy 41 ThrThrCysSerIleProGlnPheGluIleGluAsnValaAsnValaGluCysLeuAlaLeu 60
Db 121 ACCACATGCTTATTTCCACAGTTTGAAATCGAAATCGCAACGTCGAAATGCTGGCACTC 180
Qy 61 LeuLeuHisGluTyrglyTyrglyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
Db 181 CTCTTCATGAGTATTATGAGACATCGCTGGCTGGGCTGACATTAAGCATCTTTGAA 240
Qy 81 AsnMetAsnLeuAgtThrLeuSerGluLysAlaArgAspAspMetLysLysSerGln 100
Db 241 AACATGAACCTGCACAACTCTCGAGAGAGCAGCGGATGACATGAATAAAATTTCAAA 300
Qy 101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGlnGluIleSerGlnAla 120
Db 301 GCTATGACAGAAAGGTGTCACAGCCAGACAGACAGAAACAGAAATTTCCACAGCT 360
Qy 121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGlnGlyHisGlyGlyAspThr 140
Db 361 ATGAAACAAGAGAGGTGCACAGCAGCAGAGACAGAAACAGACATGGAGGACACA 420
Qy 141 TrpAspTyrglySerHisValMetThrLysPheAlaGluGluGluAspValaArgAspSer 160
Db 421 TGGGACTACAGAGAGTCACTGTATGACCAAAATTCCTGAGGAGAGATGTACGTCTAGT 480
Qy 161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
Db 481 TTGAAACACATGCTGCTGACGTGGCGGAAATGCAAGATGGCTGGGCTTTGATTTCA 540
Qy 181 AspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLys 200
Db 541 GACCGGTGGGGCTTCGGGCTCGCACGGGTGTTCTGCACGGAAGTCAAGAAATGGGAAA 600
Qy 201 SerAlaLeuAlaArgGluLeuValLeuCysTrpAlaGlnGlyGlyLeuTyrglnGlyMet 220
Db 601 TCGGCTCTAGCCACAAGAGATGCTGTGCTGGGCGCAAGGTGACCTCTACACAGGAATG 660
Qy 221 PheSerTyrglyAlaPhePheLeuProValaArgLumetGlnArgLysLysGluSerSerVal 240
Db 661 TTCTCTACAGTCTTCTCTCTCCGTTAGAGATGACGCGGAAGAGAGAGACAGTCTC 720
Qy 241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValaThrGluIleMetSer 260
Db 721 ACAAGATTCACTCCAGGAGTGGCCAGACTCCACAGGCTCGGATGACGAGATCATGTCC 780
Qy 261 ArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsn 280
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Qy 281 AsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProPheThrLeuIleArg 300
Db 841 AATGACACAAAGCTCTCCAAAGACTGGGCTGAGAGAGAGCTCGTTCCACCTCATAGCC 900
Qy 301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValaThrValaArgAspVal 320
Db 901 AGTCTGTGAGAGAGTCTGCTCTCCAGAGCTCTTCTGTATCTGACCCGACAGAGAGCTG 960
Qy 321 GlyThrGluLysLeuLysSerGluValaLysProArgTyrglyLeuLeuValaArgLysIle 340
Db 961 GGCACAGAGAACTCAAGTCAAGAGTGTGTCTCCGTTACCTGTTAGTGAAGAAATC 1020
Qy 341 SerGlyGluGlnArgGlyLeuLysLeuLeuGluLysGluLysGlyLysGlnLysThr 360
Db 1021 TCCGGGAAACAAGAAATCCACTTCTCTGAGGCGGGATGGTGAAGCATCAAGAACACA 1080
Qy 361 GlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValaProAla 380
Db 1081 CAAGGTTGGCGTGCATATGAACAACGTGAGCTGCTCCAGCCAGTCCAGTCCCGGCC 1140
Qy 381 ValGlySerLeuIleCysValaAlaLeuGluLysAspValaLysGlyLysSerVala 400
Db 1141 GTGGGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Qy 401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
Db 1201 CCTTCACCAACAAAGCTCACAGGCTGTCACGCGCTTTGTGTTTCATCAGCTCACCCCT 1260
Qy 421 ArgGlyValaValaArgArgCysLeuAsnLeuGluGluLysValaValaLysLysPheCys 440
Db 1261 CGAGCGTGTGCTCGGCTGCTCTCAATCTGAGGAAAGATGTGCTCGAAGCGCTTCTGC 1320
Qy 441 ArgMetAlaValaGluGlyValaLysAsnArgLysSerValaPheAspGlyAspAspLeuMet 460
Db 1321 GGTATGGCTGTGAGGAGGTGAGATGAAGTCAAGTGTGATGATGATGATGATGATGATG 1380
Qy 461 ValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisSmeAsnIleLeuLeuPro 480
Db 1381 GTTCAGAGATCCGGGAGTGTGAGCTCCGTCTCTGTTTCAATGAACATCTTCTCCCA 1440
Qy 481 AspSerHisCysGluGluTyrglyThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
Db 1441 GACAGCCACTGTGAGAGTACTACACTTCTTCCACTCACTCACTCACTCACTCACTCACT 1500
Qy 501 AlaLeuTyrglyValaLeuGluGluGluGluGluProAlaLeuCysProLeuTyrglyVal 520
Db 1501 GCTTGTACTACGTGTGAGAGGCTGGAATCGAGCCAGCTCTCTCCCTGTACTGCTT 1560
Qy 521 GlyLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp 540
Db 1561 GAGAAACAAAGAGTCTACATGAGCTTAAACAGCAGGCTTCCATATCCACTCGCTTTGG 1620
Qy 541 MetLysArgPheLeuPheGlyLeuValaSerGluAspValaArgArgProLeuGluValaLeu 560
Db 1621 ATGAAGCGTTTCTTGTGGCTCTGTGAGCGAAGACCTAAGAGAGGCACTGAGAGTCTG 1680
Qy 561 LeuGlyCysProValaProLeuGlyValaLysGlnLysLeuHisSerTrpValaSerLeuLeu 580
Db 1681 CTGGGCTGTCCCTTCTCCCTGGGGGTGAACAGAAAGCTTCTGCACTGGGCTCTCTGTG 1740
Qy 581 GlyLysGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPhe 600
Db 1741 GGTACGACGCTAATGCAACACCCACAGAGACACCTGACGCTTCCACTGTCTTTTC 1800
Qy 601 GluThrGlnAspLysGluPheValaArgLeuAlaLeuAsnSerPheGlnGluValaTrpLeu 620
Db 1801 GAGACTCAAGACAAAGATTGTTCCTGTGCAATTAACAGCTTCCAAAGAGTGTGCTT 1860
Qy 621 ProIleAsnGlnLeuLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrg 640
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Db 1861 CCGATTACAGAACCTGAACTTATGACATCTTCTGCTTCAGACATGTCGGTAT 1920  
Qy LeuArgLysIleArgValAspValIleGlyIlePheProArgAspGlySerAlaIle 660  
Db 1921 TTGGCGAAAATTCGGGTGATGATCAAGGATCTTCCCAAGATGATGATCCGCTAGGCA 1980  
Qy CysProValIleProLeuTrpMetArgAspIleLeuIleGluGluTrpGluAsp 680  
Db 1981 TGTCTGTGTCCTCTATGATGCGGGAATAGACCTCATGAGAGACAGTGGGAAGAT 2040  
Qy PheCysSerMetLeuGlyThrHisProHisIleuArgGlnLeuAspLeuGlySerIle 700  
Db 2041 TTCCTGCTCAATGCTTGACCCACCCACCTGCGGACCTGGACCTGGCGACGATC 2100  
Qy LeuThrGluArgAlaMetIleThrLeuCysAlaIleLeuArgHisProThrCysIle 720  
Db 2101 CTGACAGCGGGCCATAGACCTGTGTGCAAGCTGAGGCACTCCACCTGCAAGATA 2160  
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Db 2161 CAGACCTGATGTTTAAAGATGACAGATTACCTCTGTGTGACACCTCGAGAAATC 2220  
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Db 2401 TCCCCAGCCCTGAATCTCTAGGCTGGCAGAGAAACAAGTGAACAGACAGGAGTAAATG 2460  
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Qy CysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaIleuValSerAsnArgSer 860  
Db 2521 TGTGGCATCAACGACCAAGGTTGCCAGATCTGGCTCAGCCCTGTCAGACACCGAGC 2580  
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Db 2641 CGATTCAGAGGCTTCCCACTGATGTCAGAGGCTGATGCAAGTCAAGTCCACCTG 2700  
Qy AspThrAlaGlyCysGlyPheLeuAlaIleuMetGlyAsnSerTrpLeuThrHis 920  
Db 2701 GACACGGCTGCTGTGTTTCTTGCACTTGCCCTTAATGAGTAACTCATGGCTGACGAC 2760  
Qy LeuSerLeuSerMetAsnProValGlnAspAsnGlyValLysLeuLeuCysGlyIleuMet 940  
Db 2761 CTGAGCCTTAGACAGAACCTGTGGAAGACATGGCGTGAAGCTTCTGTGAGAGTCAAG 2820  
Qy ArgGluProSerCysHisIleuGlnAspLeuGluLeuValLysCysHisIleuThrAlaIle 960  
Db 2821 AGAAGAACATCTTGTCATCTCAAGGACCTGAGGTGTGAAGTGCATCTCAACCCCGC 2880  
Qy CysCysGluSerLeuSerCysValIleSerArgSerArgHisIleuLysSerLeuAspLeu 980  
Db 2881 TGTCTGTAGATCTGTCTGTGTATCTCGAGAGCAACACTTAAAGACCTGATCTTC 2940  
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Db 2941 ACGGACATGCGCTGTGGTGAACGATGGGTTGCTGTGCTGAGAGGACTGAAGCAAAAG 3000

Qy AsnSerValIleuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysGly 1001  
Db 3001 AACAGTGTTCAGAGACCTCGGGTTGAAGGATGTCATGCACTTCAATGCTGTGAG 3060  
Qy AlaIleuSerLeuAlaIleuSerCysAsnArgHisIleuThrSerLeuAsnLeuValGlnAsn 1021  
Db 3061 GCATCTCTCTTGCCCTTCTTGCAACCGGATCTGACAGCTTAACCTGTGTGAGAT 3120  
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Db 3121 AACTCACTCCCAAGAGATATGAAGCTGTGTGCGCTTGCTGTGCCAGCTTAAC 3180  
Qy LeuGlnIleIleGlyLeuTrpLysTrpIleTrpProValGlnIleArgLysLeuGlu 1080  
Db 3181 TTACAGATTAATGGCTGTGAAATGACAGTACCTGTGCAAAATAGAGAGCTGTGAG 3240  
Qy GluValGlnLeuLeuLysProArgValAlaIleAspGlySerTrpHisSerPheAspGlu 1100  
Db 3241 GAAGTGACGTAATCAACCCCGAGTCTTAATGACGCTAGTGGCATTTCTTGATGA 3300  
Qy AspAspArgHisLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCys 1120  
Db 3301 GATGACGACCAAAATGACCTTAATCTTCCGCTCCCTGAAGAGCCGGCAATGCAATGT 3360  
Qy AlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAsp 1140  
Db 3361 GCTTGTCTGTGGGATTAACCCAGAGCAAGAAAGCTGTGTCTGCTTCTGCTGAGAC 3420  
Qy PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyIleSer 1160  
Db 3421 TTCAAGAGCAGTAACGATTTGCCAAGTCTCTGCTGCGCAACCGCAATGCTGATGC 3480  
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Db 3481 CAGAGATTGAACAAGTGAACAAGCTCCCGCAACCAATGCGAGGACGGAACAACA 3540  
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Db 3601 GGGCTGTGATCAACAGTGTGATCATGACACCGAGGTATGGCTGTCTCACTAGGAGA 3660  
Qy GluLeuSerSerArgGlyLeuCysProThrValLeuMetThrThrAlaValCysProGly 1240  
Db 3661 GAGCTGAGCTGAGGGGCTGTGTGTCCAACAGTGTGATGACACAGCGGTGTCTGTGT 3720  
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Db 3721 CACTGGAGCGGCTGGGCTTGAAGGCTGTGTCTTAACAGTGTGATGAACACAGCGGT 3780  
Qy ValSerTrpSerLeuGlyAlaAlaGlyLeuGluLysLeuValSerAsnSerAlaAspAsp 1280  
Db 3781 GTGTCTGTGATCACTGGAGCGGCTGGCTGCAAGGGGCTGTGTCCAACAGTGTGATAC 3840  
Qy HisSerGlyValAlaTrpSerLeuGlyAlaAlaGlyLeuGluLysLeuValSerAsnSer 1300  
Db 3841 CACAGCGGTGTGGCTGTGCTCACTGGAGCGGCTGGGCTGTGTGTCTTCCAAACGT 3900  
Qy AlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuVal 1320  
Db 3901 GCTATGACCAACAGGGGTGTCTGTGTGATCTGGAGGAGGCTGGGCTGAGGGCTGTG 3960  
Qy SerAsnSerAlaAspAspHisSerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGlu 1340  
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RESULT 2  
US-10-066-521-5  
; Sequence 5, Application US/10066521  
; Publication No. US2003002757A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Wang, Welye  
; APPLICANT: Blatcher, Maria  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
; FILE REFERENCE: 0734-334001  
; CURRENT APPLICATION NUMBER: US/10/066,521  
; CURRENT FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: 60/318,645  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/265,231  
; PRIOR FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 4035  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(4032)  
; US-10-066-521-5

## Alignment Scores:

Pred. No.:	0	Length:	4035
Score:	1344.00	Matches:	1344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	14	Indels:	0
		Gaps:	0

US-10-066-521-6 (1-1344) x US-10-066-521-5 (1-4035)

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QY      21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGlnSer 40
Db      61 CTAGACAAGAGAAATTTCAACATTCAGAAATTTACTAAAGAAATTTCTTCAAGATCG 120

QY      41 ThrThrCysSerLierProGlnPheGlnLysLeuLeuLysLeuLysLeuLysLeuLys 60
Db      121 ACCACATGCTCTATTTCCACAGTTGAAATTCAGAAATTCAGAAATTCGCTGCACTC 180

QY      61 LeuLeuHISGluTyrgLysLysSerLeuLysLeuLysLeuLysLeuLysLeuLysLeu 80
Db      181 CTCTTGCAATGAGTATTTAGAGCATCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY      81 AsnMetAsnLeuArgThrLeuSerGluLysLysLysLysLysLysLysLysLysLys 100
Db      241 AACATGAACCTGCAACCCCTCTCGAGAGAGGCAACGAGATGACATGAAAAAATTTCA 300

QY      101 AlaMetGluGlnGluGluLysLysLysLysLysLysLysLysLysLysLysLysLys 120
Db      301 GCTATGGAACAAGAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 360

QY      121 MetGluGlnGluGluLysLysLysLysLysLysLysLysLysLysLysLysLysLys 140
Db      361 ATGGAACAAGAGGTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420

QY      141 TrpAspTyrgLysSerHisValMetThrLysPheAspLeuLysLysLysLysLysLys 160
Db      421 TGGAGCTACAGAGTCAGCTGATGACAAATTCGCTGAGAGAGAGAGAGAGAGAGAGAG 480

QY      161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
Db      481 TTGAAACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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QY      181 AspArgTrpGlyPheArgProArgThrValValLeuHISGlyLysSerGlyLysGlyLys 200
Db      541 GACCGGTGGGGCTTCCGGCTTCGACAGTGGTCTGACAGGAAAGTCAGGAATGGGAAA 600

QY      201 SerAlaLeuAlaArgGlyLysValLeuCysTrpAlaGlnGlyLysLeuTyrgLysLys 220
Db      601 TCGGCTCTAGCCAGAAAGATCGTGTCTGCGGCGGAGGTGGACCTTACAGAGATG 660

QY      221 PheSerTyrgValPhePheLeuProValArgGluMetGlnArgLysLysLysSerVal 240
Db      661 TTCTCTACGCTCTTCTCTCTCCGCTTAGAGATGACGCGAAGAGAGAGAGAGAGAG 720

QY      241 ThrGlnPheLysSerArgLysTrpProAspSerGlnAlaProValThrGluLysMetSer 260
Db      721 ACAGAGTTCACTCCAGAGGATGGCCAGACTCCAGGCTCCGGTGAAGAGATCATGCTGC 780

QY      261 ArgProGluArgLeuLeuPheLysLysLysLysLysLysLysLysLysLysLysLys 280
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QY      281 AsnAspThrLysLysCysLysAspTrpAlaGluLysGlnProPheThrLeuLysArg 300
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QY      301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuLysValThrValArgAspVal 320
Db      901 AGTCTGCTGAGGAAGCTGCTGCTCTCTGAGTCTCTGATCGTCAACGCTCAGAGAG 960

QY      321 GlyThrGluLysLeuLysSerGluValLysSerProArgTyrgLeuLeuValArgGlyLys 340
Db      961 GGCACAGAGAGAGCTCAAGTCAAGAGTGTGTCTCCGCTTACCGTTAGTTAGAGGATC 1020

QY      341 SerGlyGluGlnArgLysLysLysLeuGlnLysArgGlyLysGlyLysLysLysLys 360
Db      1021 TCCGGGAAACAAGATTCACCTTCTCTGAGGCGGGATGAGTGCATCAGAAAGCA 1080

QY      361 GlnGlyLeuArgAlaLysMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
Db      1081 CAAGGTTGGGTGGTGCATCAGAACACACGTCGAGCTGCACAGCAGTCCAGAGTCCGCG 1140

QY      381 ValGlySerLeuLysCysValAlaLeuGlnLeuGlnAspValValGlyLysSerValAla 400
Db      1141 GTGGGCTCTCTCACTCTCGTGGCCCTGACGTGACGAGCAGTGGGAGAGAGTGTGCC 1200

QY      401 ProPheAsnGlnThrLeuThrGlyLeuHISAlaAlaPheValPheLysGlnLeuThrPro 420
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QY      421 ArgGlyValValArgArgCysLeuAsnLeuGlnLysValValLeuLysArgPheCys 440
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QY      441 ArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
Db      1321 CGTATGCTGTGGAGGAGTGTGAATGGAAGTCACTGTTGATGATGAGTCACTCATG 1380

QY      461 ValGlnGlyLeuGlyLysGlnLeuArgAlaLeuPheHISMetAsnLysLeuLeuPro 480
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QY      481 AspSerHisCysGluGluTyrgTyrgThrPhePheHISLeuSerLeuGlnAspPheCysAla 500
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QY      521 GluLysThrLysArgSerMetGluLeuLysGlnAlaLysLysLysLysLysLysLysLys 540
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Qy 561 LeuGlyCysProValProLeuGlyValIlySerGlnLysLeuHisTrpValSerLeuLeu 580  
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Qy 621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640  
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; Sequence 3, Application US/10416642  
; Publication No. US20040043452A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: ARVIZU, Chandra  
; TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-0842 PCT  
; CURRENT APPLICATION NUMBER: US/10/416,642  
; CURRENT FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: 60/249,407  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 3489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1  
US-10-416-642-3  
Alignment Scores:  
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Score: 1006.00 Matches: 1006  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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## RESULT 4

US-10-216-645-1  
; Sequence 1, Application US/10216645  
; Publication No. US20030125282A1  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, BERTRAM  
; APPLICANT: LESSL, MONIKA  
; APPLICANT: PETERS-KOTTIG, MICHAEL  
; APPLICANT: BECKMANN, GREGOR  
; TITLE OF INVENTION: HUMAN MATER PROTEINS  
; FILE REFERENCE: SCH-1910  
; CURRENT APPLICATION NUMBER: US/10/216,645  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 3926  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-216-645-1

Alignment Scores:  
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Score: 1006.00 Matches: 1006  
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Query Match: 74.85% Indels: 0  
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US-10-066-521-6 (1-1344) x US-10-216-645-1 (1-3926)

Qy 98 ILeSerGlnAlaMetGluGlnGluGlyValAlaThrAlaAlaGluThrGluGluGlnGluIle 117

Db 454 ATTTCAGAGCTATGGAAACAAGAGGTCCACAGACGACAGACAGAAACAAGAAATT 513  
Qy 118 SerGlnIaMetGluGlnGluGluYAlaThraIaIaGluThrgluGlnGlnGly 137  
Db 514 TCACAGCTATGGAAACAAGAGGTCCACAGACGACAGACAGAAACAAGAGCATGGA 573  
Qy 138 GlnAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGluGluAspVal 157  
Db 574 GGTGACACATGGGACTCACAAGAGTCACGTGATGACCAAAATTCGTGAGAGAGAGATGTA 633  
Qy 158 ArgArgSerPheGluuAsnThrAlaIaAspTrpProGluMetGluInThrLeuAlaGlyAla 177  
Db 634 CGTGTAATTTTGAACACATGCTGCTGATGCTGGCCGGAATGCAACACGTGAGTGTCT 693  
Qy 178 PheAspSerAspArgTrpGlyPheAspProArgThrValValLeuHisGlyLysSerGly 197  
Db 694 TTTGATTGACACCGGTGGGCTTCGGCTCCGACCGGTGGTTCGACAGAAAGTCAGGA 753  
Qy 198 IleGlyLysSerAlaLeuAlaArgArgIleValLeuCyTrpAlaGlnGlyGlyLeuTyr 217  
Db 754 ATTGGAATCGGCTCTAGCCAGAGAGATCGTGTGCTGGCGCCAGAGTGGACTTAC 813  
Qy 218 GlnGlyMetPheSerTyrValPhePheLeuProValaArgGluMetGlnaArgLysGlu 237  
Db 814 CAGGAATGTTCTCTACGCTCTTCTCTCCCGTTAGAGAGATGCAAGCAGAGAGAGAG 873  
Qy 238 SerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGlu 257  
Db 874 AGCAGTGTACAGAGTTCAATCTCCAGAGAGTGGCCAGACTCCAGGCTCCGTTACCGAG 933  
Qy 258 IleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277  
Db 934 ATCATGTCCTCCAGCAAGAGGCTGTTGTTCAATTCATTCAGGTTTCAGAACCTGGGCTCT 993  
Qy 278 ValLeuAsnAspAspThrLysLeuCyTrpAspTrpAlaGluLysGlnProProPheThr 297  
Db 994 GTCTCAACAATGACACAAGAGCTGCAAGACTGGGCTGAGAGACACCTCCGTTACCC 1053  
Qy 298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317  
Db 1054 CTCATACGCAATCTCTGAGGAAGTCTGTCTCCCTGAGTCTTCTGATGTCACCGTCC 1113  
Qy 318 ArgAspValGlyThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuVal 337  
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Qy 338 ArgGlyLysSerGlyGluGlnArgIleHisLeuLeuGluArgGlyIleGlyGlnHis 357  
Db 1174 AGAGGAATCTCCGGGGAACAAGAAATCCACTTGTCTTGAGCGCGGAGTTGGTAGCAT 1233  
Qy 358 GlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCySerGln 377  
Db 1234 CAGAAAGACAAAGGTTGCGTCCGATCATGAAACAACCTGAGCTCTGACCAAGTCCAG 1293  
Qy 378 ValProAlaValGlySerLeuIleCyValAlaLeuGlnLeuGlnAspValValGlyGlu 397  
Db 1294 GTGCCCGCGTGGGCTCTCATCTGCGTGGCCCTGCAGCTGCAGAGAGTGGTGGGAG 1353  
Qy 398 SerValAlaProPheAsnGlnInThrLeuThrGlyLeuHisAlaIaPheValPheHisGln 417  
Db 1354 AGCGTGGCCCTTCACAACAACGCTCACAGGCTGCAGCGCGCTTTGTGTTCATCAG 1413  
Qy 418 LeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValValLeuLys 437  
Db 1414 CTCACCCCTCAGAGCGGTGCTCGCGCTGTCTCATCTCGAGAGAAAGTGTCTTGAG 1473  
Qy 438 ArgPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGlyAsp 457  
Db 1474 CGCTTCTGCGTATGCGTGTGGAAGGAGTGTGAATAGAGATGATGTTTGGAGGTAC 1533  
Qy 458 AspLeuMetValGlnGlyLeuGlyGlyuSerGluLeuArgAlaLeuPheHisMetCAsnIle 477  
Db 1534 GACCTCATGTTCAGAGACTCGGGAGATGTAGAGTCCCGTGTCTGTTCATATGAAATTC 1593

Qy 478 LeuLeuProAspSerHisCySerGluGluTyrTyrThrPhePheHisValSerLeuGlnAsp 497  
Db 1594 CTCTCCCAAGACAGCCACTGTGAGAGATGACTACACTTCTTCCACCTCAGTCTCCAGAG 1653  
Qy 498 PheCysAlaIaLeuTyrTyrValLeuGluGlyLeuGluIleGluProAlaLeuCyAspPro 517  
Db 1654 TTCTGTCCCGCTTGTACTAGTGTATAGGGGCTGTGAATGAGCCAGCTCTGTGCCCT 1713  
Qy 518 LeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHis 537  
Db 1714 CTGTACCTTGAGAGACAAAGAGTCCATGAGCTTAAACAGGAGCTTCCATATCCAC 1773  
Qy 538 SerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValaArgArgProLeu 557  
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Db 1834 GAGGTCCGTGGGCTGTCCCGTCCCTGGGGGTGAAGAGAAAGTTTGTGACTGGAGTC 1893  
Qy 578 SerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHis 597  
Db 1894 TCTGTGTGGGTCAAGACCTTAATGCCACACCCCAAGAGACACCTTGAGCCTTCAC 1953  
Qy 598 CysLeuPheGluTrpGlnAspLysGluPheValaArgLeuAlaLeuAsnSerPheGlnGlu 617  
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Qy 618 ValTrpLeuProIleAsnGlnAsnLeuAspLeuIleIleAspSerPheCySerLeuGlnHis 637  
Db 2014 GTGTGGCTTCGATTAACAGAACTTGAACTTGATTAACATTTCTTCTGTGCTCCAGAC 2073  
Qy 638 CysProTyrLeuAspGlyIleArgValAspValLysGlyIlePheProArgAspGlySer 657  
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Qy 658 AlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGln 677  
Db 2134 GCTGAGGCAATGCTCGTGTGTCCCTGTATGATGGGAGTAAGACCTCATTAAGAGAGACAG 2193  
Qy 678 TrpGluAspPheCysSerMetLeuGlyThrHisProHisValLeuArgGlnLeuAspLeuGly 697  
Db 2194 TGGGAAGATTTCTGCTCATGTGAGCTTGGCAACCCACACCTGCGGAGCTGAGCTGAGC 2253  
Qy 698 SerSerIleLeuThrGluArgAlaMetLysThrLeuCyValaLysLeuArgHisProThr 717  
Db 2254 AGCAGCATCTCGACAGACGGGGCCATGAACCTGTGTGCCAAGCTGAGGCACTCCAC 2313  
Qy 718 CysLysIleGlnInThrLeuMetPheArgAsnAlaGlnIleThrProGlyValaGlnHisLeu 737  
Db 2314 TGCAGATACAGACCTGATGTTAAGAAATGCAAGATTAACCTGTGTGTGCACACTTC 2373  
Qy 738 TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeu 757  
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Qy 758 LysGluGluAspValaArgMetAlaCySerGluAlaLeuLysHisProLysCysLeuLeuGlu 777  
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Qy 778 SerLeuArgLeuAspCysCySerGlyLeuThrHisAlaCyTyrLeuLysIleSerGlnIle 797  
Db 2494 TCTTTAGGGCTGATGCTGTGATTAACCATGCTGTTAACTGAAGATCTCCAAATC 2553  
Qy 798 LeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValaThrAspGln 817  
Db 2554 CTTACGACCTCCCACTGAATCTCTGAGCTGTGCAGGAAACAAGGTGACAGACAG 2613  
Qy 818 GlyValMetProLeuSerAspAlaLeuArgValaSerGlnCysAlaLeuGlnValLeuIle 837  
Db 2614 GAGATTAATGCTCTCAAGTATGCTTGAAGATTCACAGTGGCGCTGCAGAAAGCTGATA 2673



QY 838 LeuGluAapCySgLyIleThrAlaThrGlyCySgInSerLeuAlaSerAlaLeuValSer 857  
Db 2674 CTGAGAGACTGTGGCATCAAGCCAGCGGTTGCCAGAGTCTGGCCCTCAAGCCCTGTCAAGC 2733  
QY 858 AsnArgSerLeuThrHisLeuCySgLeuSerAsnAsnSerLeuGlyValAsnGlyValAsn 877  
Db 2734 AACCGAGCTTGAACACCTGTGCTTATCCAAACACCTGGGGAAGAGAGTGAAT 2793  
QY 878 LeuLeuCySgSerMetArgLeuProHisCySgSerLeuGlnArgLeuMetLeuAsnGln 897  
Db 2794 CTACTGTCTCATCATAGAGCTTCCCACTGTATCTGCAAGAGCTGATGCTGAATCAG 2853  
QY 898 CySgHisLeuAapThrAlaGlyCySgLyPheLeuAlaLeuAlaMetGlyValAsnSerTrp 917  
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QY 918 LeuThrHisLeuSerLeuSerMetAsnProValGluAapAsnGlyValIleLeuLeuCyS 937  
Db 2914 CTGACGCACTGAGGCTTGAACATGAACCTGTGAAGCAATGGGCTGAAGCTTGTGTC 2973  
QY 938 GluValMetArgGluProSerCySgHisLeuGlnAapLeuGluLeuValIleCySgHisLeu 957  
Db 2974 GAGGTCAATGAAGAACATCTTGTATCTCAAGACCTGAGAGTGTGAAGTGTATCTC 3033  
QY 958 ThrAlaAlaCySgCySgLeuSerLeuSerCySgValIleSerArgSerArgHisLeuLySer 977  
Db 3034 ACCGCGGCTGTGTGAGAGTCTGTCTGTGTGATCTGAGAGAGCAACCTGAAGAGC 3093  
QY 978 LeuAapLeuThrAspAsnAlaLeuGlyAapGlyValAlaAlaLeuCySgGlyLeu 997  
Db 3094 CTGATCTCAAGCAATAGCCCTGGGTGACGATGGGTTGGCTGCACTGTGCAAGGAGCTG 3153  
QY 998 LysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCySgGlyLeuThrSerAsp 1017  
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QY 1058 ThrSerLeuLeuGlnIleIleGlyLeuThrPheSerTrpGlnTrpProValGlnIleArgLys 1077  
Db 3334 ACGTCTAACTTAAGATTAATGGCTGTGAATGGCAAGTACCTGTCAATTAAGAGAG 3393  
QY 1078 LeuLeuGluGluValGlnLeuLeuLysProArgValValIleAapGlySerTrpHisSer 1097  
Db 3394 CTGCTGAGAGAGTGCAGCTACTCAAGCCCGAGTCTAATTGAAGTATGATTTGCAATCT 3453  
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Db 3454 TTTGATGAAGATGACCGG 3471

RESULT 5  
US-10-216-645-3

; Sequence 3, Application US/10216645  
; Publication No. US20030125282A1  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, BERTRAM  
; APPLICANT: LESSL, MONIKA  
; APPLICANT: PETERS-KOTTIG, MICHAEL  
; APPLICANT: BECKMANN, GEORG  
; TITLE OF INVENTION: HUMAN MATER PROTEINS  
; FILE REFERENCE: SCH-1910  
; CURRENT APPLICATION NUMBER: US/10/216,645  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 3  
; LENGTH: 3830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-216-645-3  
Alignment Scores:  
Pred. No.: 0 Length: 3830  
Score: 988.00 Matches: 988  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 73.51% Indels: 0  
DB: 15 Gaps: 0  
US-10-066-521-6 (1-1344) x US-10-216-645-3 (1-3830)  
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QY 136 HisGlyGlyAapThrTrpAspTrpLysSerHisValMetThrLysPheAlaGluGluGlu 155  
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QY 196 SerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCySgTrpAlaGlnGly 215  
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QY 276 GlySerValLeuAsnAsnAspThrLysLeuCySgLyAspTrpAlaGluLysGlnProPro 295  
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QY 396 GlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPhe 415

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Qy 496 GlnAspPheCysAlaAlaLeuTyrTyrValLeuGluGlyLeuGluValLeuProAlaLeu 515  
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Qy 576 TyrValSerLeuLeuGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAla 595  
Db 1831 TGGGCTCTCTGTGGGTGAGACGCTTAATGCCACCACTCCAGAGAGACCTTGAGCC 1890  
Qy 596 PheHisCysLeuPheGlnThrGlnAspLysGlnPheValArgLeuAlaLeuAsnSerPhe 615  
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Qy 616 GlnGluValTyrLeuProIleAsnGlnAsnLeuAspLeuIleAsnSerPheCysLeu 635  
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Qy 636 GlnHisCysProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAsp 655  
Db 2011 CAGCACTGTCCGATTTCGGAATAATTCGGGTGATGTCAAAAGGATCTTCCAAAGAT 2070  
Qy 656 GlnSerAlaGlnAlaCysProValValProLeuTyrMetCysArgAspLysThrLeuIleGlu 675  
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Qy 696 LeuGlySerSerIleLeuThrGlnArgAlaMetLysThrLeuCysAlaLysLeuArgHis 715  
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Qy 716 ProThrCysLysAlaIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGln 735  
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Qy 736 HisLeuTyrArgGlyValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyThr 755  
Db 2311 CACCTCTGGAAGATGTCTATGCGCAACCGTAACCTAAGATCCCTCAACTTGGAGGAC 2370  
Qy 756 HisLeuLysGlnGluAspValArgMetAlaCysGlnAlaLeuLysHisProLysCysLeu 775

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Db 2491 CAAATCCTTACGACCTCCCGAGCCTGAATACTGTGAGCCCTGGAGAAACAAAGTGA 2550  
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Qy 876 ValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeu 895  
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Qy 976 LysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGln 995  
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Qy 996 GlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThr 1015  
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Qy 1036 AsnLeuValGlnAsnAsnPheSerProLysGlyMetLeuLysLeuCysSerAlaPheAla 1055  
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Qy 1056 CysProThrSerAsnLeuGlnIleIleGlyLeuThrLysTyrPheGlnTyrProValGlnIle 1075  
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Qy 1076 ArgLysLeuLeuGlnGlnValGlnLeuLeuLysProArgValValIleAspGlySerTyr 1095  
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Qy 1096 HisSerPheAspGlnAspAspArg 1103  
Db 3391 CATCTTTGTATGAAGATGACCGG 3414

RESULT 6  
US-10-092-900A-347  
; Sequence 347, Application US/10092900A

Publication No. US20040043382A1  
GENERAL INFORMATION:  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Taupier Jr., Raymond J.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Li, Li  
APPLICANT: Zernusen, Bryan D.  
APPLICANT: Gusev, Vladimir Y.  
APPLICANT: Ji, Weizhen  
APPLICANT: Gorman, Linda  
APPLICANT: Miller, Charles E.  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Paturajan, Meera  
APPLICANT: Gangoli, Beha A.  
APPLICANT: Verne, Corine A.M.  
APPLICANT: Guo, Xiaojia Sasha  
APPLICANT: Tchernev, Valizar T.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Liu, Yi  
APPLICANT: Anderson, David W.  
APPLICANT: Spaderma, Steven K.  
APPLICANT: Carterton, Elina  
APPLICANT: Leite, Mario W.  
APPLICANT: Zhong, Haihong  
APPLICANT: Alsbrook, John P.  
APPLICANT: Lepley, Denise M.  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Burgess, Catherine B.  
TITLE OR INVENTION: NO. US20040043382A1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-290C  
CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: USN 60/274,322  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USN 60/283,675  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: USN 60/338,092  
PRIOR FILING DATE: 2001-12-03  
PRIOR APPLICATION NUMBER: USN 60/274,281  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USN 60/274,191  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USN 60/325,681  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: USN 60/304,354  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: USN 60/279,995  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: USN 60/294,899  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: USN 60/287,424  
PRIOR FILING DATE: 2001-04-30  
Remaining Seq ID Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 768  
SEQ ID NO 347  
LENGTH: 3226  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (69)..(3168)  
US-10-092-900A-347

Alignment Scores:  
Pred. No.: 0  
Score: 968.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%

Length: 3226  
Matches: 968  
Conservative: 0  
Mismatch: 0

Query Match: 72.02% Indels: 0  
DB: 17 Gaps: 0  
US-10-066-521-6 (1-1344) x US-10-092-900A-347 (1-3226)  
QY 136 HIGLYGIAPPTHTTPAPTLYLYSSEHISVALNETHHTLYPHEALAGLUGLU 155  
DB 249 CATGAGGTGACACATGGACTACAGAGTACCGTAGATGACCAATGCTGAGAGAG 308  
QY 156 AAPPVALARGASERPEHGLUANTHPLAALAPPTTPROGLUMETGLTHREULA 175  
DB 309 GATGACGTGCTGATGTTTGAACACCTGCTCTGACGCGGAATGCAACGTTGCT 368  
QY 176 GLVALPHEAPSERAPARTPTGPLYPHEARPROAGTHTVALLEUHIISGLIYYS 195  
DB 369 GGTCTTTTGAATTCAGACCGGTGGGCTCCGGCTCGACAGTGTCTTCACGGAAG 428  
QY 196 SERGLYIIEGLYYSERIALALEUALARGHRTILEALLUENCYETPPLAGLNGLY 215  
DB 429 TCAGGAATTGGGAATCGGCTCTAGCCAGAGATCGTGTGCTGGCGCAAGTGA 488  
QY 216 LEUTYTGNGLYMECPHESETTYTVALPHEHEUPROVALARGLUIMETGLNARGYS 235  
DB 489 CTTAACCGGGAATGTTCTCTACGCTTCTCTCCCGTTAGAGATGACGAGAG 548  
QY 236 LYSGLUSERSERVALTHRGUPLHEILSEERAGLUPTTPROAPSERGLNALAPROVAL 255  
DB 549 AAGAGACATGTCACAGATTCTCCAGGAGTGGCCAGACTCCACGGCTCCGGTG 608  
QY 256 THRGUIMETSERATGPROGLUARGLEUPHEILEILEAPGLYPHEASAPLEU 275  
DB 609 ACGGAGATCATGTCCCGACAGAAAGGCTGTTCATCATTTGACGGTTGATGACCTG 668  
QY 276 GLYSERVALLEUANAASAPHTHTLYSEUCYSYASPTTPALAGLUYGLIPROPRO 295  
DB 669 GCTCTGCTCCCAACAAGACAAAGCTGTGCAAGCTGGCTGAGAACACAGCTCCG 728  
QY 296 PHERHTLEUILEATGSRLEULEUARGLYSVALLEUENUPROGLUSERPHELEULEVAL 315  
DB 729 TTCACCTCATACGACGCTCTCTAGAGAGTCTGCTCTCTGAGTCTTCTCATGCTC 788  
QY 316 THRYVALARGAPVALIGLYTHRGULYSLEULYSERGLUVALISERPROAGTYTLEU 335  
DB 789 ACCGTCAGAGACGTTGGGACAGAGAGTCAAGTCAAGGTCGTTGCTCCCGTTACCTG 848  
QY 336 LEUVALARGGLYIIESERGLYGLUINARGTLEHISLEULEULEUARGLYIIEGLY 355  
DB 849 TTAGTTAGAGGAATCTCCGGGGAACAAGATCCACTTGTGAGCGCGGATTTGCT 908  
QY 356 GLIHIGLILYSTRHNGLYLEUARGALILEMETASNAASAPRGJULEULEUAPGLN 375  
DB 909 GAGCATTCAGAGACACAAAGGTTGCTGTCATGACATGAAACCGTAGCTCTGACAG 968  
QY 376 CYSGLINVALPROALAVAGLYSERLEUIECYSVALALALEUGINLEUGINASPVAL 395  
DB 969 TGCAGAGTCCCGCGCTGCTCTCATCTGCGTGGCCCTGCAAGTGTGAGAGTGTG 1028  
QY 396 GLYGLUSERVALAPROPHESERGLNTHREUTHRGLYLEUHSALALPHEVALPHE 415  
DB 1029 GGGGAGAGCGTCCCTCTCAACCAACGCTCACAGGCTCGACGCGCTTTGTGTGT 1088  
QY 416 HIGLILYSTRHNGLYLEUARGVALVALARGARGYSEULEUENUGLUGUARGVAL 435  
DB 1089 CATGACGTCAACCTTCAGAGGCTGTGCTGCTGCTCAATTCAGAGAAAGTTGTC 1148  
QY 436 LEULYSARGPHECYARGMETALAVAGLUGLYVALTRPANAARGLYSERVALPHEAP 455  
DB 1149 CTGAAGCGCTTCTGCGATGCTGTGAGGAGATGTGGAATAGAGTCACTTTTAC 1208  
QY 456 GLYASAPLEUETVALINGLYLEUGLYLEUGLYLEUARGALALEUPHEHMET 475  
DB 1209 GGTGACACATCATGTTCAAGAGACTCGGAGAGTGTGAGTCTCGTGTTCACATG 1268

Qy 476 Asn11eLeuLeuProAspSerHisCySGluGluTyrTyrThrPhePheHisLeuSerLeu 495  
Db 1269 AAGATCCTTCTCCAGACAGACAGCTGTGAGGAGTATCAACCTTCTTCCACTCAGTCTC 1328  
Qy 496 GlnAspPheCySA1aAlaLeuTyrTyrValLeuGluGluLeuGluLeuGluProAlaLeu 515  
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Qy 516 CySProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHis 535  
Db 1389 TGCCCTCTGTAGTGTGAAGAACAAGAGGTCCATGAGGCTTTAAACAGGAGGCTTCAT 1448  
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Db 1449 ATCCACTGCTGTGTGATGACGGTTCCTGTGTGCTCGTGAAGGAGGATGAAGAGG 1508  
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Qy 576 TrpValSerLeuLeuGluGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAla 595  
Db 1569 TGGGCTCTCTGTGTGGGTCAACAGCCTTAATGCAACCCAGAGAGACCCCTGAGCGCC 1628  
Qy 596 PheHisCySAleuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPhe 615  
Db 1629 TTCCACTGCTCTTTCGAGACTCAAGACAAAGAGTTTTCCTGTGCTGTGCTGTGCTGTG 1688  
Qy 616 GlnGluValTrpLeuProIleAsnGlnAsnLeuLeuIleAlaSerSerPheCyLeu 635  
Db 1689 CAAGAAGGTGGCTTCCGATTAAACAGAACCTGAGCTGTGATGACATCTTCTGCTCTC 1748  
Qy 636 GlnHisCyProTyrLeuArgLysIleArgValAspValLysGlyLysPheProArgAsp 655  
Db 1749 CAGACCTGTCCGTATTGCGGAAATTCGGGTGATGATCAAGAGATTTCCCAAGAGAT 1808  
Qy 656 GluSerAlaGluAlaCySProValProLeuTyrMetArgAspLysThrLeuIleGlu 675  
Db 1809 GAGTCCGCTGAGGAGATGTCTGTGTCTCTATGATGCGGATTAACCTCCTCATTTAG 1868  
Qy 676 GluGlnTrpGluAspPheCySerMetLeuGlyThrHisProHisLeuArgGluLeuAsp 695  
Db 1869 GAGCAGTGGAGAAATTTGTCTCCATGCTTGACCCACCCACCTGCGGAGCTGAGC 1928  
Qy 696 LeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCySA1aLysLeuArgHis 715  
Db 1929 CTGGGACAGACATCTTCAAGAGGCGCATGAAGACCTGTGTGCCAATCTAGGAT 1988  
Qy 716 ProThrCySA1aLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGln 735  
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Qy 736 HisLeuTyrArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyLysThr 755  
Db 2049 CACCTGTGAAATGTATGATGCGCAACCGTAACTTCAACTTGTGAGGAGCC 2108  
Qy 756 HisLeuLysGluGluAspValArgMetAlaCySGluAlaLeuLysHisAspProLysCySerLeu 775  
Db 2109 CACCTGAAAGAAAGATGATGAAGATGCGCTGAGACCTTAAACACCCCAAAATGTTTG 2168  
Qy 776 LeuGluSerLeuArgLeuAspCySGlyLeuThrHisAlaCyTyrLeuLysIleSer 795  
Db 2169 TTGAGGTCTTGAAGGCTGATGCTGTGATGATGACCCATGCTGTACTGAAGATCTCC 2228  
Qy 796 GlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThr 815  
Db 2229 CAAATCTTACGACTCCCGCAGACCTGAAATCTCGAACCTCGGACGAGAAACAGTGCA 2288  
Qy 816 AspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCySA1aLeuGlnLys 835  
Db 2289 GACCAAGGAGATATGCTCTCAAGTATGCTTGAAGAGTCTCCCAAGTGGCCCTGACAGAG 2348  
Qy 836 LeuIleLeuGluAspCySGlyLysThrAlaThrGlyCySGlnSerLeuAlaSerAlaLeu 855

Db 2349 CTGATCTGAGAGACTGTGGCATCAAGACCGGCTTGCCAGAGTGTGGCTCAGCCCTC 2408  
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Qy 896 AsnGlnCyHisLeuAspThrAlaGlyCySGlyPheLeuAlaLeuMetGlyAsn 915  
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Db 2589 TCATGGCTGAGCAGCCTGAGCCTTATGATGAACCTGTGGAAGCAATGGGTAACTT 2648  
Qy 936 LeuCySGluValMetArgGluProSerCyHisLeuGlnAspLeuGluLeuValLysCyS 955  
Db 2649 CTGTGCGAGGTCAATGAGAAACATCTTGTATCTCCAGAGCCTGAGTTGTGTAAAGTGT 2708  
Qy 956 HisLeuThrAlaAlaCySGlySerLeuSerCySA1aLysSerArgHisLeu 975  
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Qy 996 GlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCySGlyLeuThr 1015  
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Qy 1016 SerAspCySGlyValAlaLeuSerLeuAlaLeuSerCySAAsnArgHisLeuThrSerLeu 1035  
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Qy 1096 HisSerPheAspGluAspArg 1103  
Db 3129 CATCTTTGTATGAAGATGACCGG 3152

RESULT 7  
US-10-860-761-3  
: Sequence 3, Application US/10860761  
: Publication No. US2004024875A1  
: GENERAL INFORMATION:  
: APPLICANT: WYETH  
: TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS  
: FILE REFERENCE: AM101318  
: CURRENT APPLICATION NUMBER: US/10/860,761  
: CURRENT FILING DATE: 2004-06-03  
: NUMBER OF SEQ ID NOS: 31  
: SOFTWARE: PatentIn version 3.2  
: SEQ ID NO: 3  
: LENGTH: 3885  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: CDS

LOCATION: (1) ... (3603)  
US-10-860-761-3

## Alignment Scores:

Align. No.: 0 Length: 3885  
Score: 616.00 Matches: 1002  
Percent Similarity: 99.21% Conservative: 0  
Best Local Similarity: 99.21% Mismatches: 4  
Query Match: 45.83% Indels: 8  
DB: 18 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-860-761-3 (1-3885)

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Qy 118 Sersglnalameglunglunlglualarhralaalagluthrglunglunlglue 137
Db 628 TCACAAAGCTATGGAACAAAGAGTGTCCACAGACAGACAGACAGACAAAGAAATGGA 687
Qy 138 GLYAPRTTTPAPRTTTPAPRTTTPAPRTTTPAPRTTTPAPRTTTPAPRTTTPAP 157
Db 688 GGTGACATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 747
Qy 158 Argatserpnegluasnthralaalaprtpproglumetglnthreulalaglula 177
Db 748 CTTCTATGTTTGAACAAAGTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 807
Qy 178 Pheapseraspargtrpdllyphearproarhtrhvalleuhsaglylysergyl 197
Db 808 TTTGATTCAGACCGGTGGGCTTCCGGCTCGACCGTGTGTCTGACAGAAAGTCAGGA 867
Qy 198 Ileglylysserhaleuhalargarglilevalleuqsttrpalaglunlglunlglue 217
Db 868 ATTGGAATCGGCTGTAGCCAGAGAGATCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 927
Qy 218 Glnnglymetpaserftrvalphepheleuprovalargglumetglnthreulalagl 237
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Qy 358 Glnlyserthrnglunlglunlgluephelelleleaprglypheapshleuglyser 377
Db 1348 CAGAAAGACAAAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1406
Qy 377 nvalproalavalgllyserleulleqcyavalalaleuqglunlglunlglue 397
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Qy 437 YSARGPheCyBarghnealavalaglunlglunlgluephelelleleaprgly 457
Db 1586 AGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1645
Qy 457 SPASpLeuMeCyValGlnlglunlglunlgluegluserglnleuarglaleuphehsme 477
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Qy 477 leleuueuproapserserhscysglunlglunlgluephelelleleaprgly 497
Db 1706 TCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1765
Qy 497 APpHeCyAlalaleuqcyalyasaprtpralaglulysglnprophether 517
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Qy 537 leserleuqcyalyasaprtpralaglulysglnprophether 557
Db 1886 ACTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1945
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Qy 597 leserleuqcyalyasaprtpralaglulysglnprophether 617
Db 2066 ACTGTCTTTCGAGAGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2125
Qy 617 lualthrleuqcyalyasaprtpralaglulysglnprophether 637
Db 2126 AAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2185
Qy 637 leserleuqcyalyasaprtpralaglulysglnprophether 657
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Db 2306 AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2365
Qy 697 luserleuqcyalyasaprtpralaglulysglnprophether 717
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Qy 737 eutprarglilevalmeclalasnarganleuargserleuqcyalyasaprtpralagl 757
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Db 2546 TGAAGAGAGAGATGTAAGATGGCGTGTGAAGCCTTAAACACCCAAAGTTTGTGG 2605  
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Db 2666 AGCTTTAAGGCTGATTCGTGTGATGTAAGCCCATGCTGTTACTGAAAGATCTCCAA 2665  
Qy 797 TLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspG 817  
Db 2666 TCTTACAGACCTCCCGCAGCTGAAATCTCTGAGCTGCGAGAAACAAGGTGACAGACC 2725  
Qy 817 TnglyValMet-ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeu 836  
Db 2726 AGGGATGAC-GCCCTCAGTATGCTTGAAGGCTCCCAAGTGGCCCTGAGAGCTG 2784  
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Db 2785 ATACGAGAGACTGTGGCATCAGACCCAGGTTCCAGAGTCTGGCTCAGCCCTCGTC 2844  
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Qy 916 TTrpleuThrHisLeuSerLeuSerMetAsnProValGlnAspAsnGlyValLysLeuLe 936  
Db 3024 ATGGCTGACGACCTGAGCCTTAGATGATGACCTGTGAAAGCAATGGCGTAGCTTCT 3083  
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Qy 976 sSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGlnG 996  
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Qy 996 YLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSe 1016  
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Qy 1096 sSerPheAspGlnAspAspArg 1103  
Db 3564 TTCTTTTATGATGATGACCGG 3585

RESULT 8  
US-10-399-443-23

; Sequence 23, Application US/10399443  
; Publication No. US20040028669A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute  
; APPLICANT: Health  
; APPLICANT: Nelson, Lawrence M.  
; APPLICANT: Tong, Zhi-Bin  
; APPLICANT: Nelson, Lawrence  
; APPLICANT: Zhi-Bin, Tong  
; TITLE OF INVENTION: Human Gene Critical to Fertility  
; FILE REFERENCE: 4239-64785  
; CURRENT APPLICATION NUMBER: US/10/399,443  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/241,510  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: PCT/US01/10981  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 3900  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3600)  
; OTHER INFORMATION:  
US-10-399-443-23  
  
Alignment Scores:  
Pred. No.: 0 Length: 3900  
Score: 616.00 Matches: 1002  
Percent Similarity: 99.21% Conservative: 0  
Best Local Similarity: 99.21% Mismatches: 4  
Query Matchn: 45.83% Indels: 8  
Gaps: 0  
17  
  
US-10-066-521-6 (1-1344) x US-10-399-443-23 (1-3900)  
Qy 98 TleSerGlnAlaMetGlnGlnGlnGlyAlaThrAlaAlaGlnThrGlnGlnGlnLutle 117  
Db 568 ATTTCACAGACTATGAAACAAGAGGTGCCACAGCAGACAGACAGAAACAAGAAATT 627  
Qy 118 SerGlnAlaMetGlnGlnGlnGlyAlaThrAlaAlaGlnThrGlnGlnGlnGlyHisGly 137  
Db 628 TCACAGACTATGAAACAAGAGGTGCCACAGCAGACAGACAGAAACAAGAAACAATGGA 687  
Qy 138 GlyAspThrTrpAspTrpLysSerHisValMetThrLysPheAlaGlnGlnGlnAspVal 157  
Db 688 GGTACACATGGGACTCAAGAGATCACGTGATGACCAAAATTCGCTGAGAGAGAGATGTA 747  
Qy 158 ArgArgSerPheGlnAsnThrAlaAlaAspTrpProGlnMetGlnThrLeuAlaGlyVala 177  
Db 748 CGTGTGATTTTGAACAACACTGTGCTGACTGCGCGGAAATGCAACGTTGGCTGTGCT 807  
Qy 178 PheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGly 197  
Db 808 TTTGATTCAGACCGGTGGGCTTCCGCTCGACAGGTGTCTTCGACAGAAATCTCAGA 867  
Qy 198 TleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyGlyLeuTr 217  
Db 868 ATGGGAAATCGGCTTAGCAGAAAGATGTGCTGTGCTGGCGCAAGGTGGACTTAC 927  
Qy 218 GlnGlyMetPheSerTrpValPhePheLeuProValArgGlnMetGlnArgLysGlyGlu 237  
Db 928 CAGGAAATGTTCTCTACGCTTCTTCTCCCTTGAAGAGTGCAGCGGAAAGAGAG 987  
Qy 238 SerSerValThrGlnPheIleSerArgGlnTrpProAspSerGlnAlaProValThrGlu 257  
Db 988 AGCAGTGTACAGAGTTCATTCAGGAGAGTGGCAGACTCCAGGCTCCGCTGACGAG 1047  
Qy 258 TleMetSerArgProGlnArgLeuPheIleIleAspGlyPheAspAspLeuGlySer 277

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Db 1048 ATCATGTCGCCGACGAAAGCGCTGTGTTCATCATTCGAGGTTTCGATGACCTGGGCTCT
Qy 278 ValLeuAsnAspThrIleuCyAlaAspTPrAlaGluValProProPheThr
Db 1108 GTCCCTCAACAAATGACCAAGAGCTGTGCAAGAGCTGGAGAGAGCTTCGGTTCACC
Qy 298 LeuIleAspSerLeuLeuArgIleValIleuLeuProGluSerPheLeuIleValThrVal
Db 1168 CTCATACCAAGCTCTCTAGAGAGAGCTTCCTTCCTTCATTCCTCAACCGTC
Qy 318 ArgAspValGlyThrGluValLeuValSerProArgTyrLeuLeuVal
Db 1228 AGAGACGTGGGACAGAGAGCTCAAGTCAAGAGTGTGTCTCCCGTTACCTGTATAGT
Qy 338 ArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgIleGlyGlnHis
Db 1288 AGAGAAATCTCCGGGAAACAAAGAAATCCATTGCTCTTGACCGGGAGTTGGTAGCAT
Qy 358 GlnValThrGlnGlyLeuArgAlaIleMet-AsnAsnArgGluLeuLeuAspGlnCysGln
Db 1348 CAGAAAGACAAAGGTTGCTGTCGATCAT-CAACAACTGAGCTGCTGACCAAGTCCA
Qy 377 nValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGly
Db 1407 GGTGCCCCCGGTGGCTCTCATCTGCGTGGCCCTGACGCTGACAGAGCTGGTGGGGA
Qy 397 uSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal-PheHisG
Db 1467 GAGCTCTCCCGCTTCACAAACGCTCAAGCGCTGACCGCGCTTTTGGC-GTTTCATC
Qy 417 IleLeuThrProArgGlyValAlaArgArgCysLeuAsnLeuGlnGluArgValValLeu
Db 1525 GAGCTCTCCCGCTTCACAAACGCTCAAGCGCTGACCGCGCTTTTGGC-GTTTCATC
Qy 437 yAspArgPheCysArgMetAlaValGluGlyValTPrAsnArgIleSerValPheAspGly
Db 1586 AGCGCTTCGCGGTGCTGTGAGAGGAGTGTGAATAGAAAGTCAAGTGTGATGGTG
Qy 457 sPheAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsn
Db 1646 AGCACTCATGTTGACAAAGACTCGGGAGTCTGAGACTCGTCTGTTTCCATGAACA
Qy 477 IleLeuLeuProAspSerHisCysGlnGluGlyTyrTyrThrPhePheHisLeuSerLeuGln
Db 1705 TCTCTTCCCAAGACGACCTGTGAGAGTACTACCTTCTTCCACCTCAAGTCTCCAG
Qy 497 sPheCysAlaAlaLeuTyrTyrValIleGluGluGluIleGluProAlaLeuCysP
Db 1766 ACTTCTGTGCGGCTGTGACTAGCGTTAGAGGCGCTGGAAATCGAGCAGCTCTGCG
Qy 517 roleuTyrValGluValThrIleValArgSerMetGluLeuValGlnAlaGlyPheHisIleH
Db 1826 CTCTGTAGTGTGAGAAAGCAAAAGAGTGCATGAGCTTAAACAGCAGGCTTCCATATCC
Qy 537 IAspSerLeuThrMetIleValArgPheLeuPheGlyLeuValSerGluAspValArgAspPro
Db 1886 ACTGCTTGTGAGTGAAGCGTTCGTGTGTGCTGTGAGCGAACAAGTGAAGAGCCAC
Qy 557 euGluValIleLeuGlyCysProValProLeuGlyValIleGlnIleLeuHisIleTPrV
Db 1946 TGGAGGTCTCTGCGGCTGTCCCGTTCCTCGGGGTGAAGAGAGCTTCTGCACTGG
Qy 577 aIleSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheH
Db 2006 TCTCTCTGTGGGTGACAGCTTAATGCCACCAACCCAGAGAGACACCTTGAGCGCTTCC
Qy 597 IAspValLeuPheGlnThrGlnAspIleValPheValArgLeuAlaLeuAsnSerPheGlnG
Db 2066 ACTGCTTGTGAGACTCAAGCAAAAGAGTGTGTGCTGTGCACTTAAACAGCTTCCAG
Qy 617 IuValTPrLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnH

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Db 2126 AAGTGTGGCTTCGATTAACAGAACTGGACTGTATGACATCTTCTGCTCCAGC
Qy 637 IAspProTyrIleuArgIleValAspValIleGlyIlePheProArgAspGlnS
Db 2186 ACTGTCCGATTTGGGGAATTCGGGTGGATGTCAAGAGATCTTCCAAAGATGAGT
Qy 657 eArgAlaIleCysProValValProLeuTPrMetArgAspIleThrLeuIleGluGlnG
Db 2246 CCGTGAAGGAGATGCTCTGTGGTCCCTATGATGATCGGGATAGAACCTCATTTAGAGAGC
Qy 677 IITPrGluAspPheCysSerMetLeuGlyThrHisProHisIleuArgIleLeuAspLeuG
Db 2306 AGTGGAAAGATTTCTGCTCCAGCTTGGACCCACCAACCTGGGAGCTGGACCTGG
Qy 697 IYSerSerIleLeuThrGlnArgAlaMetIleValThrCysValAlaValLeuArgHisP
Db 2366 GCAGAGATCTTGACAGAGCGGGAGAGAACCTGTGTCCAAAGCTGAGGAGATCCCA
Qy 717 hrCysValIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHis
Db 2426 CCGCAAGATACAGACCTGATGTTAGAAATGACAGATTAACCTGGTGTGCAACACC
Qy 737 eUTPrArgIleValIleAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisI
Db 2486 TCTGGAGATGCTGTATGGCCAACTTAACCTTAAGATCCCTCAACTTGGGAGGACCCACC
Qy 757 euIleGluGluAspValArgMetAlaCysGluAlaLeuValHisPProIleCysLeuLeuG
Db 2546 TGAAGAAAGAGATTAAGAGAGGTGTGAAGCTTAAACCCAAATATTTGTTGG
Qy 777 IuSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrIleuValIleSerGlnI
Db 2606 AGCTTTGAGGTGATGCTGTGTGATGACCAAGCTGCTGTTACCTGAAGATCTCCCAA
Qy 797 IleLeuThrThrSerProSerLeuIleValSerLeuLeuAlaGlyAsnValIleThrArg
Db 2666 TCTTTACCACTCCCGGAGCTGAATCTGAGCTGGACGCTGGAGAAACAGGTGACAGACC
Qy 817 IuGlyValMet-ProLeuSerAspAlaLeuArgValIleGlnCysAlaLeuGlnIleVal
Db 2786 AGGAGTGAAC-GCCTCTAGTATGCTTGAAGGCTCCCAAGTGGCCCTGAGAGCTG
Qy 837 IleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuVal
Db 2785 ATACTGAGAGATGTGGATACAGACCAAGGTTGCCAGAGTCTGAGCTCCAGCTCTGCT
Qy 857 SerAsnArgSerLeuThrHisIleuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyVal
Db 2845 AGCAACCGAGCTTGACACCTGTGCTATCCAAACAAGCTGGGAAACGAAAGTGA
Qy 877 AsnLeuLeuCysValGlySerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuH
Db 2905 AATCTACGTGTGTGATCATGATAGGCTTCCCACTGTATCTGCAAGAGCTGATGTGAT
Qy 897 GlnCysHisIleuAspThrAlaGlyCysGlyPhe-LeuAlaLeuAlaLeuMetGlyAsnSe
Db 2965 CAGTGCACCTTGAGACAGCGGTGGCTGTGG-TTCTTTTCACTTGGCTTATGGGTAATC
Qy 916 ITPrLeuThrHisIleuSerLeuSerMetAsnProValGluAspAsnGlyValIleValLeu
Db 3024 ATGGCTGACGACCTGAGACCTTGAAGTGAACCTGTGAAAGCAATGGCGTGAACCTTCT
Qy 936 uCysGlyValMetArgGluProSerCysHisIleuGlnAspLeuGluLeuValIleValCysHis
Db 3084 GTGCGAGGTGTATGAGAAACATCTTGTCACTTCAGAGACCTGAGGTGTGAATGTCA
Qy 956 sLeuThrAlaAlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisIleuVal
Db 3144 TCTCAACCGCGGTGCTGTGAGATCTGTCTGTGTATCTCGAGAGACCAAGACCTTGA
Qy 976 sSerLeuAspLeuThrArgAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlnI
Db 3204 GAGCTGATCTCAACGAGCAATGCGCTGTGAGCGGTGGCTGTGCGTGTGAGAGG

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QY 996 YLeuLysGluLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSe 1016  
Db 3264 ACTGAAGCAAAAGAAAGAGTGTCTGACGAGACTGGGTTGAAGGACATGTGACTGACTTC 3323  
QY 1016 rAspCysGlySerGluAlaLeuSerSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAs 1036  
Db 3324 TGATGCTGTGAGGAGCACTCTCTTGGCCCTTTCGCAACCGGCACTTGACCAAGCTTAA 3383  
QY 1036 nLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaC 1056  
Db 3384 CTTGGTGAAGAAATTAATTCACTCCCAAGAGATGAGCTGTGTTGGCTTTGGCTTG 3443  
QY 1056 sProThrSerAsnLeuGlnIleIleGlyLeuThrLysTrpGlnTrpProValGlnIleAr 1076  
Db 3444 TCCACGCTAACTTACAGATTAATTGGGCTGTGAAATGCGAGTACCCTGTGCAAAATAG 3503  
QY 1076 GlyLeuLeuGluGluValAlaGlnLeuLeuLysProArgValAlaIleAspGlySerTrpHi 1096  
Db 3504 GAAGCTGTGAGGAGAGTGCAGCTACTGAAGCCCGAGTCGTAAATGACGGTAGTTGCA 3563  
QY 1096 sSerPheAspGluAspAspArg 1103  
Db 3564 TTCTTTGATGAAGATGACCGG 3585

## RESULT 9

US-10-677-943-23

; Sequence 23, Application US/10677943

; Publication No. US20040072297A1

; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America as

; APPLICANT: represented by the Secretary of the Department of Health and

; APPLICANT: Human Services

; APPLICANT: Nelson, Lawrence

; APPLICANT: Tong, Zhi-Bin

; TITLE OR INVENTION: Human Gene Critical to Fertility

; FILE REFERENCE: 4239-64790

; CURRENT APPLICATION NUMBER: US/10/677,943

; CURRENT FILING DATE: 2003-10-01

; PRIOR APPLICATION NUMBER: 60/241,510

; PRIOR FILING DATE: 2000-10-18

; PRIOR APPLICATION NUMBER: PCT/US02/09776

; PRIOR FILING DATE: 2002-03-29

; PRIOR APPLICATION NUMBER: PCT/US01/10981

; PRIOR FILING DATE: 2001-04-04

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 23

; LENGTH: 3900

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3600)

US-10-677-943-23

## Alignment Scores:

Pred. No.:	0	Length:	3900
Score:	616.00	Matches:	1002
Percent Similarity:	99.21%	Conservative:	0
Best Local Similarity:	99.21%	Mismatches:	4
Query Match:	45.83%	Indels:	8
DB:	17	Gaps:	0

US-10-066-521-6 (1-1344) x US-10-677-943-23 (1-3900)

QY 98 lLeSerGlnAlaMetGluGluGluGlyAlaThrAlaAlaGluThrGluGluGlnGluIle 117  
Db 568 ATTTCACAAAGCTATGGAACAAGAGGTGCCACAGACAGACAGACAGAAACAAGAAATT 627  
QY 118 SerGlnAlaMetGluGluGluGluGlyAlaThrAlaAlaGluThrGluGluGlnGlyHiGly 137  
Db 628 TCACAAAGCTATGGAACAAGAGGTGCCACAGACAGACAGACAGAAACAAGAAACAATTGA 687

QY 138 GlyAspThrTrpAspTrpLysSerHisValMetThrLysPheAlaGluGluAlaAspVal 157  
Db 688 GGTGACACATGGAGCTACCAAGAGTCAAGTATGACCAAAATTCGTGAGAGAGAGATGTA 747  
QY 158 ArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAla 177  
Db 748 CGTGATGTTTTGAAAACAATGCTGTGATCGGCGGAAAGCAAAAGCTGTGGTGGCT 807  
QY 178 PheAspSerAspArgTrpGlyPheArgProArgThrValAlaLeuHisGlyLysSerGly 197  
Db 808 TTTGATTCAGACCGAGTGGGCTTCCGGCTTGCACCGGTGTCTTCACGAGAAATCAGGA 867  
QY 198 lLeGlyLysSerAlaLeuAlaArgArglLeValLeuCysTrpAlaGlnGlyLysLeuTr 217  
Db 868 ATTGGAATATGGCTCTAGCCAGAAAGATCGTGTGCTGGGCGCAAGGTGACTTAC 927  
QY 218 GlnGlyMetPheSerTrpValPhePheLeuProValArgGluMetGlnArgLysGlu 237  
Db 928 CAGGAAATGTTCTCTACGCTCTCTCTCTCCCTTGAAGAGTCAAGCGGAAAGAG 987  
QY 238 SerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGlu 257  
Db 988 AGCAGTGTACAGATTCATCTCAGAGAGTGGCCAGATCCAGGCTCCGCTACAGAG 1047  
QY 258 lLeMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySer 277  
Db 1048 ATCATGTCCGACCAAGAAAGCTGTGTTCATCATTTGACGGTTTCGATGACCTGGGCTCT 1107  
QY 278 ValLeuAsnAsnAspThrLysLeuCysLysAspTrpAlaGlyGlnProProPheThr 297  
Db 1108 GTCTTCAACATGACAAAGACTGTGCAAGACGTGGCTGAAAGACGCTCCCTTCAACC 1167  
QY 298 LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317  
Db 1168 CTGATAGCACTGTCTGAGAGAGTCTCTGCTCCCTTGAAGTCTTCTGATGTGACCGTC 1227  
QY 318 ArgAspValGlyThrGluLysLeuLysSerGluValAlaSerProArgTrpLeuLeuVal 337  
Db 1228 AGAAGCGTGGGACAGAAAGACTCAAGTCAAGAGTGTGTCTCCCGTTACCTGTAGTT 1287  
QY 338 ArgGlyLysSerGlyGluGlnArglLeHisLeuLeuLeuGluGlylLeGlyGluHis 357  
Db 1288 AGAGAAATCTCCGGGGAACAAGATCACTGTCTCTTGAAGCCGGGATTTGGAGACAT 1347  
QY 358 GlnLysThrGlnGlyLeuArgAlaIleMet-AsnAsnArgGluLeuLeuAspGlnCysG 377  
Db 1348 CAGAAACACAAAGGTGTGCTGCATCAT-CAACACCGTAGCTGCTCGACCACTGCCA 1406  
QY 377 nValProAlaValGlySerLeuIleCysValAlaLeuGlnAspValValGlyG 397  
Db 1407 GGTGCGCGCGTGGGCTCTGCATCTGCTGGCCCTGACGTGACAGACGAGTGGGGA 1466  
QY 397 uSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheVal-PheHisG 417  
Db 1467 GAGCGTGGCCCTTCAACCAAGCTCACAGGCTTCACAGCCGCTTTTGC-GTTTTATC 1525  
QY 417 lLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluAlaArgValAlaLeu 437  
Db 1526 AGCTCACCCCTTCAGGGGTGTCCGGCGCTGTCTCAATCTGAGAGAAAGATTGTCTG 1585  
QY 437 yAspPheCysArgMetAlaValGluGlyValTrpAsnArgLysSerValPheAspGly 457  
Db 1586 AGGCTTCTGGCGATGCTGTGAGAGGAGTGTGAATGAGAACTGATGATGTTG 1645  
QY 457 sPAspLeuMetValGlnGlyLeuGlyGluSerGluLeuAspAlaLeuPheHisMetAsn 477  
Db 1646 ACGACTTCATAGTTCAGAGACTCGGGGAGTCTGAGCTCCGCTCTCTTTCACATGAAACA 1705  
QY 477 lLeuLeuProAspSerHisCysGluGluTrpTrpPhePheHisLeuSerLeuGln 497  
Db 1706 TCTTTCCTCCAGACAGCACTGTGAGAGTACTACACTTCTTCCACTGACTCCAGG 1765



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; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-1

Alignment Scores:
Pred. No.: 0          Length: 1157
Score: 385.00        Matches: 385
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 28.65%  Indels: 0
DB: 17          Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-1 (1-1157)
QY 252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGly 271
Db 1 CAAAGCTCCGGTGAAGAGATCATGTCCGACCAAGAAAGGCTGTGTTTCATCATTTGACGGT 60
QY 272 PheAspAspLeuGlySerValIleuAsnAsnAspThrIlySleuCySlyAspTrpAlaGlu 291
Db 61 TTCGATGACCTGGGGCTGTCTCTCAACAATGACAAAGCTCTGCAAAAGACTGGGGCTGAG 120
QY 292 LysGlnProProPheThrIleuIleArgSerIleuAspGlyValLeuLeuProGluSer 311
Db 121 AAGGAGCCTCCGTTCAACCTCATACGCACTGCTGAGAGAGGCTCTGCTCCAGAGTCC 180
QY 312 PheLeuIleValThrValArgAspValGlyThrGluIlySleuSergIuValIleSer 331
Db 181 TTCCTGATCGTCAACGTCAGAGACGTGGGCAAGAGAGCTTCAAGTCAAGAGGTGTCT 240
QY 332 ProArgTyrLeuLeuValArgGlyIleSergIyGluGlnArgIleIleSleuLeuGlu 351
Db 241 CCCCGTTACCTGTTAGTTAGAGGATCTCCGGGGAACAAAGATCACTTCTCCTTGAG 300
QY 352 ArgGlyIleGlyGluHisGlnIlySthrGlnIlyLeuArgAlaIleMetAsnAsnArgGlu 371
Db 301 CGCGGAGTTGGTGGACATCAGAAAGACAAAGGCTGTGCGATCATGAAACACCTGAG 360
QY 372 LeuLeuAspGlnIySthrGlnIleValProAlaValGlySergIleuIleCySValAlaLeuGlu 391
Db 361 CTGCTCGACAGTGCAGGTGCGCGCGTGGCTCTCTCATCTGGGTGCGCTGAGTGTG 420
QY 392 GlnAspValValGlyGluSerValAlaIleProPheAsnGlnThrLeuThrGlyIleuHisAla 411
Db 421 CAGGACCGTGGTGGGGAGAGGCGTCCGCCCTTCAACCAAGAGCTACAGGCGCTGAGCC 480
QY 412 AlaPheValPheHisGlnLeuThrProArgIyValValAlaArgArgCySLeuAsnLeuGlu 431
Db 481 GCTTTTGTGTTTCATCAGCTCAACCTCGAGGCGGTGTCGGGCGCTGTCTCAATCTGGAG 540
QY 432 GlnArgValValIleuIlyValArgPheCySArgMetAlaValGluGlyValThrAsnArgIys 451
Db 541 GAAAGAGTGTCTCGAAAGCGCTTCTGCGGTATGGTGGAGGAGGTGTGAATAAGAGAG 600
QY 452 SerValPheAspGlyAspAspLeuMetValGlnIlyLeuGlyGluSergIuLeuArgAla 471
Db 601 TCAAGTGTGAACGGGAGGACCTCATGTTCAAGGACCTCGGGAGCTCGAGCTCCGTCCT 660
QY 472 LeuPheHisMetAsnIleLeuLeuProAspSerHisCySgIuGlyIyTyrTrpPhePhe 491
Db 661 CTGTTTCACATGAACATCTCTCTCCAGACAGCCACTGAGAGTACTTACACCTTCTTTC 720
QY 492 HisIleuSergIleuGlnAspPheCySValAlaLeuIyTyrValIleuGlnGlyIleuGluIle 511
Db 721 CACCTCACTCTCCAGGACTTCTGTGCGCGCTTGTATCAAGGTATGAGAGGCGCTGAAATC 780
QY 512 GlnProAlaLeuCySProLeuTyrValGluIySthrIlySAspSergMetGluIleuIysGln 531
Db 781 GAGCGACGCTCTCTGCGCTCTGTACCTTGAAGAGACAAAGAGGTCCATGAGACTTAAACAG 840
QY 532 AlaGlyPheHisIleHisSergIleuTrpMetIySArgPheLeuPheGlyLeuValSergIu 551
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Db 841 GCAGGCTTCCATATCACTGCTTTGAGTGAAGCGTTTCTTTGGCCTTCGTAGCGAA 900
QY 552 AspValArgArgProLeuGlnValIleuLeuGlyCySProValProLeuGlyValIysGln 571
Db 901 GAGCTTAAGAGAGGCCACTGAGAGGTCTCTGCTGGGCGTGTCCCGTCCCTCGGGGGTGAACAG 960
QY 572 LysLeuLeuHisGTrpValSergIleuGlyGlnIleProAsnAlaThrTrpProGlyAsp 591
Db 961 AAGCTTCTGACACTGGGTCTCTGTGGTGGTCAAGAGCCCTATATGCACACCCCAAGAGAC 1020
QY 592 ThrIleuAspAlaPheHisCySLeuPheGluThrGlnAspIySgIuPheValArgLeuAla 611
Db 1021 ACCCTGAGCGCCTTCCACTGCTCTTTTCAAGACTCAAGACAAAGAGTTGTTCGCTGGCA 1080
QY 612 LeuAsnSergPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleIleSer 631
Db 1081 TTAAACAGCTTCCAAAGAGTGTGGCTTCGATTAAACAGAACTGAGCTGATGACATCT 1140
QY 632 SerPheCySLeuGln 636
Db 1141 TCCTTGTGCTCCAG 1155

RESULT 11
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; represented by the Secretary of the Department of Health and
; Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677, 943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241, 510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-1

Alignment Scores:
Pred. No.: 0          Length: 1157
Score: 385.00        Matches: 385
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 28.65%  Indels: 0
DB: 17          Gaps: 0

US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)
QY 252 GlnAlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGly 271
Db 1 CAAAGCTCCGGTGAAGAGATCATGTCCGACCAAGAAAGGCTGTGTTTCATCATTTGACGGT 60
QY 272 PheAspAspLeuGlySerValIleuAsnAsnAspThrIlySleuCySlyAspTrpAlaGlu 291
Db 61 TTCGATGACCTGGGGCTGTCTCTCAACAATGACAAAGCTCTGCAAAAGACTGGGGCTGAG 120
QY 292 LysGlnProProPheThrIleuIleArgSerIleuAspGlyValLeuLeuProGluSer 311
Db 121 AAGGAGCCTCCGTTCAACCTCATACGCACTGCTGAGAGAGGCTCTGCTCCAGAGTCC 180
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Qy 312 PheleuileValThrValArgAspValGlyThrGlyIleuLeuYSerGluValValSer 331  
Db 181 TTCGATGTCACCGTCAGAGACGTGGGACAGAGAGCTCAAGTCAAGGTCGTCT 240  
Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeu 351  
Db 241 CCCGTTACCTGGTTAGTTAGAGAAATCTCCGGGAAACAAAGATCCATCTGCTTGA 300  
Qy 352 ArgGlyIleGlyGlnHisGlnIleThrGlnGlyLeuArgAlaIleMetAspAsnArgGlu 371  
Db 301 CGCGGATTTGGTGAACATCAGAGACAGAGGTTTGGTGGCATATGAAACACCTGAG 360  
Qy 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGln 391  
Db 361 CTGCTGCACGATGTCAGGTGCGCGCGGTGCTCTCATCTGGTGGCCCTGCAGCTG 420  
Qy 392 GlnAspValValGlyIleSerValAlaProPheAsnGlnThrThrGlyLeuHisAla 411  
Db 421 CAGACGTGGTGGGAGAGCGTCCGCCCTTCAACCAACGCTCAGAGGCTGCACGCC 480  
Qy 412 AlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlu 431  
Db 481 GCTTTGTGTTTCATCAGCTCAACCTCGAGGCGTGGTCCGGCGCTGCTCATCTGAG 540  
Qy 432 GlnArgValValLeuLeuArgPheCysArgMetAlaValGlyValTyrAsnArgIle 451  
Db 541 GAAGAGTGTCTGTAACGCTTCCGCTAGTATGCTGAGAGGAGTGTGAATGAGAG 600  
Qy 452 SerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyIleSerGluLeuArgAla 471  
Db 601 TCAGGTTTGAACGCTGACACCTCATGTTCAAGACATCGGGGAGTCTGAGCTCGTCT 660  
Qy 472 LeuPheHisMetAsnIleLeuLeuProAspSerHisCysGlnGluTyrTyrThrPhe 491  
Db 661 CTGTTTCAGACGAAATCTTCTCCAGACAGCCCTGAGAGATCTACACCTTCTTC 720  
Qy 492 HisLeuSerLeuGlnAspPheCysAlaIleuTyrTyrValLeuGlnGlyLeuGln 511  
Db 721 CACCTCACTCTCCAGGACTTCTGTGCGCGCTTGTACTAGTGTAGAGGCTGGAATC 780  
Qy 512 GlnProAlaLeuCysProLeuTyrValIleuIleThrIleArgSerMetGluLeuGln 531  
Db 781 GAGCAGCTCTCTGCTCTGCTGACCTGAGAGACAAAGAGGCTTCATGAGCTTAAACG 840  
Qy 532 AlaGlyPheHisGlnHisSerLeuThrMetLeuAspPheLeuPheGlyLeuValSerGlu 551  
Db 841 GCAGGCTTCCATATCCACTCGCTTGGATGAAGCGTTTCTGTGGCTGCTGAGCGAA 900  
Qy 552 AspValArgAspProLeuGlnValLeuLeuGlnCysProValProLeuGlyValIleGln 571  
Db 901 GACGTAGAGAGGCACTGAGGCTCTGCTGGGCTGTCCCGTTCCCTGGGGTGAAGCG 960  
Qy 572 LysLeuLeuHisIleTyrValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAsp 591  
Db 961 AAGCTTGCACATGGGTCTCTGTGGGTGAGCAGCTTAATGCCACACCCAGAGAAC 1020  
Qy 592 ThrLeuAspAlaPheHisCysLeuPheGlnThrGlnAspIleGlnPheValArgLeuAla 611  
Db 1021 ACCGTGACGCTTCCACTGCTTTCAGACTCAAGACCAAGAGATTTGCTGCTGCA 1080  
Qy 612 LeuAsnSerPheGlnGluValTyrLeuProIleAsnGlnAsnLeuAspLeuIleAlaSer 631  
Db 1081 TTAAACAGCTTCCAAAGAGTGGCTTCCGATTAAACGAACCTGCACTTATAGACTCT 1140  
Qy 632 SerPheCysLeuGln 636  
Db 1141 TCCTTCTGCTCCAG 1155

RESULT 12  
US-10-399-443-3  
; Sequence 3, Application US/10399443  
; Publication No. US20040028669A1  
; GENERAL INFORMATION:

; APPLICANT: The Government of the United States of America, as Represented by the  
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute  
; APPLICANT: Health  
; APPLICANT: Nelson, Lawrence M.  
; APPLICANT: Tong, Zhi-Bin  
; APPLICANT: Nelson, Lawrence  
; APPLICANT: Zhi-Bin, Tong  
; TITLE OF INVENTION: Human Gene Critical to Fertility  
; FILE REFERENCE: 4239-64785  
; CURRENT APPLICATION NUMBER: US/10/399,443  
; CURRENT FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: 60/241,510  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: PCT/US01/10981  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1075  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-399-443-3

Alignment Scores:  
Pred. No.: 1,19e-192 Length: 1075  
Score: 196.00 Matches: 252  
Percent Similarity: 99.21% Conserves: 0  
Best Local Similarity: 99.21% Mismatches: 1  
Query Match: 14.58% Indels: 2  
DB: 17 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-3 (1-1075)

Qy 851 LeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysGluSerAsnAspSer 870  
Db 2 CTGGCTTACGCTTCGTGACAGACCGGAGCTTGAACACCTGTGCTATCCAAACAGCG 61  
Qy 871 LeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeu 890  
Db 62 CTGGGAAACGAAGGTGTAATCTACTGTGTGATCTCAAGAGCTTCCCACTGATGCTG 121  
Qy 891 GlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLe 910  
Db 122 CAGAGGCTGATGCTGAATCACTGACCACTTGACACGGCTGCTGAG--TTCTTGGCACT 180  
Qy 910 ValAlaLeuMetGlyAsnSerTyrLeuThrHisLeuSerLeuSerMetAsnProValGlnAs 930  
Db 181 TGCCTTAATGGGTAACTCATGCTGACGACCTGAGCTTGAACCTCTGAGAAAG 240  
Qy 930 PAsnGlyValLysLeuLeuCysGlnValMetArgGluProSerCysHisLeuGlnAspLe 950  
Db 241 CAATGGCGTGAAGCTTCTGTGAGAGTCAATAGAAACATCTTGTATCTCCAGAGACT 300  
Qy 950 GlnLeuValLysCysHisLeuThrAlaAlaCysCysGlnSerLeuSerCysValIleSer 970  
Db 301 GGAATGGTAAAGTATGATATCAACGCGCGGTGCTGAGAGTCTGTCTGTGATCTC 360  
Qy 970 PArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyVal 990  
Db 361 GAGGAGCAGACACCTGAAGACCTGAGATCTCAACGACCATCTCGGGTGAACGGGGGT 420  
Qy 990 AlaAlaLeuCysGlnGlyLeuLysGlnIleAsnSerValLeuThrArgLeuGlyLeuLys 1010  
Db 421 TGTGCGGTGTGCAAGGAGTGAAGCAAAAGAGTGTGACAGACCTGGGTTGA 480  
Qy 1010 AlaCysGlyLeuThrSerAspCysCysGlnAlaLeuSerLeuAlaLeuSerCysAsnArg 1030  
Db 481 GGCATGTGAGACTGATCTGTATGCTGTGAGGCACTCTCTGAGCCCTTCTCAACCG 540  
Qy 1030 GHisLeuThrSerLeuAsnLeuValGlnAsnAspPheSerProLysGlyMetMetLysLe 1050  
Db 541 GCATCTGACAGTCTAAACCTGTGAGAAATTAATCTTACGCTCCAAAGAAATGAAGACT 600

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Qy 1050 uCyseRAlaphheAlaCyseProThrsSerAsnLeuGlnIleIleGlyLeuTrpLysIle 1070
Db 601 GTGTCGGCTTGTGCTTCCACGCTCACTTAACAGTAATGCGCTGGAATGCA 660
Qy 1070 nTyProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValVa 1090
Db 661 GTACCTGTGTGAATAAGAGAGCTGCTGAGAGAGTGAAGTCACTCAAGCCCGAGTGT 720
Qy 1090 lIleAspGlySerTrpHisSerPheAspGluAspAspArg 1103
Db 721 AATTGACGGTAGTGTGCAATCTTTGTGATGAGATGACCGG 760

RESULT 13
US-10-677-943-3
; Sequence 3, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64730
; CURRENT APPLICATION NUMBER: US/10/677,943
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-3

Alignment Scores:
Pred. No.: 1,19e-192 Length: 1075
Score: 196.00 Matches: 252
Percent Similarity: 99.21% Conservative: 0
Best Local Similarity: 99.21% Mismatches: 1
Query Match: 14.58% Indels: 2
DB: 17 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-677-943-3 (1-1075)
Qy 851 LeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuValSerAsnAsnSer 870
Db 2 CTGGGCTCAGCCCTGCTCAGACACCGAGCTTGACACACCTGCTCATCCAAACACGAC 61
Qy 871 LeuGlyAsnGluGlyValAsnLeuLeuValArgSerMetArgLeuProHisCysSerLeu 890
Db 62 CTGGGGAACGAGGCGTAATCTACTGTGATCCAGAGGCTTCCCACTGATGCTG 121
Qy 891 GlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPhe-LeuAlaLe 910
Db 122 CAGAGGCTGATGCTGAATCACTGACCACTGACACAGGCTGCTGGG-TTCTCTTGCACT 180
Qy 910 ValLeuMetGlyValAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAs 930
Db 181 TGCCCTATATGGTAACTCATGAGCTGACGCACTGAGCTTATGACATGAACCTGTGGAAGA 240
Qy 930 PAsnGlyValValysLeuLeuValCysGluValMetArgGluProSerCysHisLeuGlnAspLe 950
Db 241 CAATGGCGCTGAAGCTTCTGTGCGAGGTCATGAGAAACATCTGTCAATCTCCAGAGACT 300
Qy 950 uGluLeuValLysCysHisLeuThrAlaAlaCysGagGluSerLeuSerCysValIleSe 970
Db 301 GGAAGTTGATAAAGTCAATCTCAACGCGCGCTGTGAGAGTCTGTCTGTGATCTC 360
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Qy 970 rArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyValVa 990
Db 361 GAGAGAGAGACACCTGAAGAGCCGTGATCTCACGGAACAAGCCCTGGGTGACGCTGGGGT 420
Qy 990 lAlaAlaLeuCysGluGluGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLy 1010
Db 421 TGCTGCCCTGTGCAGGAGACTGAAAGCAAAAGAACAGTCTTCTGACGAGACTCGGGTTGAA 480
Qy 1010 sAlaCysGlyLeuThrSerAspCysGlyAlaLeuSerLeuAlaLeuSerCysAsnAr 1030
Db 481 GGCATGTGACTGACTCTTCAATGCTGTGAGGCACTCTCTTGCCCTTCTCTGCAACCG 540
Qy 1030 gHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGlyMetMetLysLe 1050
Db 541 GCATCTACCAAGTCTAAACCTGGGAGAAATTAATCTTAAGTCCCAAGAAATGATGAAGCT 600
Qy 1050 uCyseRAlaphheAlaCyseProThrsSerAsnLeuGlnIleIleGlyLeuTrpLysIle 1070
Db 601 GTGTCGGCTTGTGCTTCCACGCTCACTTAACAGTAATGCGCTGGAATGCA 660
Qy 1070 nTyProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValVa 1090
Db 661 GTACCTGTGTGAATAAGAGAGCTGCTGAGAGAGTGAAGTCACTCAAGCCCGAGTGT 720
Qy 1090 lIleAspGlySerTrpHisSerPheAspGluAspAspArg 1103
Db 721 AATTGACGGTAGTGTGCAATCTTTGTGATGAGATGACCGG 760

RESULT 14
US-10-027-632-258159
; Sequence 258159, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258159
; LENGTH: 2099
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258159

Alignment Scores:
Pred. No.: 3.52e-48 Length: 2099
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.24% Indels: 0
DB: 13 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-027-632-258159 (1-2099)
Qy 668 MetArgAspLysThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThr 687
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GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 4, 2005, 13:10:24 ; Search time 496 Seconds

(without alignments)  
4433.782 Million cell updates/sec

Title: US-10-066-521-6

Perfect score: 7074  
Sequence: 1 MBDKSLTFSSYGLQWCLYE.....DDHSGVSWSLGAGLEGLVS 1344

## Scoring table:

BIOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-Q=/cgn2\_1/USPRO.epool/h/US10066521/runat\_04022005\_114552\_4412/app\_query.fasta\_1.1543  
-DB=Issued\_Patents\_NA -QMT=fastap -SUFFIX=std.rml -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdl  
-LIST=45 -POCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10066521 @CGN\_1\_1\_107 @runat\_04022005\_114552\_4412 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	955	13.5	4422	4	US-09-388-221B-1 Sequence 1, Appli
2	949	13.4	4200	4	US-09-388-221B-3 Sequence 3, Appli
3	949	13.4	4332	4	US-09-388-221B-5 Sequence 5, Appli
4	948	13.4	4466	4	US-09-388-221B-11 Sequence 11, Appli
5	945.5	13.4	4556	4	US-09-388-221B-9 Sequence 9, Appli
6	630.5	8.9	1374	2	US-08-910-731-3 Sequence 3, Appli
7	630.5	8.9	1374	2	US-08-795-395-3 Sequence 3, Appli
8	621	8.8	1371	2	US-08-910-731-1 Sequence 1, Appli
9	621	8.8	1371	2	US-08-795-395-1 Sequence 1, Appli
10	612	8.7	1371	2	US-08-910-731-7 Sequence 7, Appli
11	607.5	8.6	1386	2	US-08-910-731-5 Sequence 5, Appli
12	406	5.7	3156	4	US-09-799-451-870 Sequence 870, App

13	379.5	5.4	4141	3	US-09-245-281-42 Sequence 42, Appli
14	379.5	5.4	4141	3	US-09-207-359B-42 Sequence 42, Appli
15	379.5	5.4	4141	3	US-09-340-620A-42 Sequence 42, Appli
16	379.5	5.4	4141	4	US-09-865-364-42 Sequence 42, Appli
17	364	5.1	4485	4	US-09-949-016-3209 Sequence 1, Appli
18	364	5.1	4485	4	US-10-014-269-1 Sequence 1, Appli
19	359.5	5.1	3382	3	US-09-099-041A-7 Sequence 7, Appli
20	359.5	5.1	3382	3	US-09-245-281-7 Sequence 7, Appli
21	359.5	5.1	3382	3	US-09-207-359B-7 Sequence 7, Appli
22	359.5	5.1	3382	4	US-09-340-620A-7 Sequence 7, Appli
23	359.5	5.1	3382	4	US-09-865-364-7 Sequence 7, Appli
24	351	5.0	4486	4	US-10-014-269-33 Sequence 33, Appli
25	347	4.9	2859	3	US-09-099-041A-9 Sequence 9, Appli
26	347	4.9	2859	3	US-09-245-281-9 Sequence 9, Appli
27	347	4.9	2859	3	US-09-207-359B-9 Sequence 9, Appli
28	347	4.9	2859	4	US-09-340-620A-9 Sequence 9, Appli
29	347	4.9	2859	4	US-09-865-364-9 Sequence 9, Appli
30	327	4.6	4543	2	US-08-519-547A-5 Sequence 5, Appli
31	319.5	4.5	4346	4	US-09-064-199-12 Sequence 12, Appli
32	319.5	4.5	4366	4	US-09-064-199-14 Sequence 14, Appli
33	319.5	4.5	4418	4	US-09-064-199-13 Sequence 13, Appli
34	319.5	4.5	4431	4	US-09-064-199-8 Sequence 8, Appli
35	319.5	4.5	4441	3	US-09-641-999-2 Sequence 2, Appli
36	319.5	4.5	4441	4	US-09-064-199-10 Sequence 10, Appli
37	319.5	4.5	4549	4	US-09-064-199-9 Sequence 9, Appli
38	319.5	4.5	4564	4	US-09-064-199-2 Sequence 2, Appli
39	319.5	4.5	4649	4	US-09-064-199-11 Sequence 11, Appli
40	319.5	4.5	4746	4	US-09-064-199-7 Sequence 7, Appli
41	319.5	4.5	5105	4	US-09-064-199-3 Sequence 3, Appli
42	319.5	4.5	5463	4	US-09-064-199-1 Sequence 1, Appli
43	309	4.4	3393	5	US-08-295-502-1 Sequence 1, Appli
44	309	4.4	3393	5	PCT-US95-10691-1 Sequence 1, Appli
45	307	4.3	4302	3	US-09-245-281-38 Sequence 38, Appli

## ALIGNMENTS

## RESULT 1

US-09-388-221B-1  
; Sequence 1, Application US/09388221B  
; Patent No. 6818750  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation  
; FILE REFERENCE: P-LJ 3650  
; CURRENT APPLICATION NUMBER: US/09/388,221B  
; CURRENT FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4422  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(4422)  
US-09-388-221B-1

## Alignment Scores:

Pred. No.:	4.57e-91	Length:	4422
Score:	955.00	Matches:	366
Percent Similarity:	38.01%	Conservative:	189
Best Local Similarity:	25.07%	Mismatches:	438
Query Match:	13.50%	Indels:	468
DB:	4	Gaps:	51

US-10-066-521-6 (1-1344) x US-09-388-221B-1 (1-4422)

QY	11	SerTYrGlyLeuGlnITrPyCysLeuTYrGlu--LeuAspYrGluGluInpGheGlnThrPhe	29
DB	13	GCTTGGGCGCCCTGCGCTGCTGTTACTTGGAGTTCCTGAGAGGAGACTGAGAGGATGTC	72
QY	30	LysGluLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe	48

Db 73 CAGCTTCTGCTGCCAATAAAGCGACTCCAGAGCTCTTCGGGTGAGACACCCGCTCAG 132  
 Oy 49 GtuitlegluasnalabnvalglucybleualaleuLeuLeuuhfsglutrytryglYala 68  
 Db 133 CCAGAGAAGACAGATGGCATGAGGGTGGCGCTGTACTGTGGCTCAG---TATGGGAG 189  
 Oy 69 SerleuAlaTPAlaThrserIleSerIlePhegluAsMetCAsleuuhrythLeuSer 88  
 Db 190 CAGCGGCTGTGACCTAGCTTACCTTACCTGGAGCAGATGGGGCTGAGGTCACTGTGC 249  
 Oy 89 GluYsAlaArgAspAsp----- 94  
 Db 250 GCCCAAGCCAGAGAAAGGGGACAGGCACTCTCCTCATTCCTTACAGCCCAAGTAACC 309  
 Oy 94 ----- 94  
 Db 310 CACGTGGGGTCTCCAGCCAACCCACCTCACCGCAGTGTATGCGCTGGATCCATGAA 369  
 Oy 94 ----- 94  
 Db 370 TTGCGGGCGGGGTGACACCGAGGCTCAGAGAGAGGGTGTGAGACGTGCTGTACACA 429  
 Oy 95 -----MetLysIleSerGlnAlaMet----- 102  
 Db 430 TCTGAGCGCGCTGAGAGAAATCTGCTCTCACTCTTACCAAGCTCTTCAGAGTCC 489  
 Oy 102 ----- 102  
 Db 490 CCAGACATGAGTCTCCAGCCAGAGTCACCCAAGGCCCAATCCACAGAGTGTG 549  
 Oy 103 -----GluGlnGluYala--- 107  
 Db 550 GGGAGCTGGGGATCCCACTCAGCCAGCTCAGCACCCAGAGAGCAGAGGCTCTGGG 609  
 Oy 108 -----ThraAlaGluThrgluGlu 114  
 Db 610 ACCCAATGGCTCTGGATGAAACGTCAAGAAATTACTACAGAAATCAGAGAAAGAG 669  
 Oy 115 GlnGlnIleSerGlnAlaMetGluGlnGluYalaThraAlaGluThrgluGln 134  
 Db 670 AGAGAGAAATCAGAGAAAGGAGGAGGCCCCATGGGCGCGGTGTAGAAACGCCCCACAG 729  
 Oy 135 GlnYhsglyY----- 138  
 Db 730 GGGCACACCAAGCTCAGCCCCACACCACTGAGGAGCTTCTGTGAGAGAGAGCTC 789  
 Oy 139 ---AspThrTTPAspTyrIleSerIhsvaIleThr---LysPhe----- 151  
 Db 790 TGTTCACATGGCCCTGGAAAATGAGATTTTAACCAAAAATTCACACAGCTGTAATT 849  
 Oy 152 -----AlaGluGlnGluAspValArgArgSerPheGluAsnThr 164  
 Db 850 CTACAAAGACCTCACCCAGAAAGCCAAAGATCCCTCGGTCAAGAGAGAC----- 897  
 Oy 165 AlaAlaAspTTPPro-----GluMetGlnThr 173  
 Db 898 -----TGGCTTGATTATGTGAGAGAGATTCAGACATTTAATTAGATTCAGAGAC 948  
 Oy 174 LeuAlaGly---AlaPheAspSerAspArgTTPGlyPheArgProArgThraValLeu 192  
 Db 949 TTATTGGCCCAAGGCTGATACCCA-----GAACCTCGCATATGATCATACTAG 996  
 Oy 193 HisGlyLysSerGlyIleGlyLysSerIleAlaAlaArgArgIleValLeuYserTPAla 212  
 Db 997 CAGGGGGCTGCTGGAAATGGGAAGTCACACTGGCCAGGAGTGAAAGAGACCTGGGGG 105  
 Oy 213 GlnGlyGlyLeuYtryGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232  
 Db 1057 AGAGGCCAGCTTAATGGGAGCCGCTTCCAGCAGTCTTACTTCAAGCTCAGAGAGCTG 1111  
 Oy 233 GlnArgLysLysGluSerValThrgluPheIleSerArgLysGluTTPProAspGln 252

Db	1117	GCCAGCTCAGAAAGGTGTAGTCTGGCTGAGCTACCTGGAAGAAAGATGGGACAGCACTCCG	1176
Qy	253	AlAProValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspArgIlePhe	272
Db	1177	GCTCCATTAACAGATCTGTCTGTACAGGCGAGCGAGCTCTTCATCTGATGGTGTGA	1236
Qy	273	AspArgLeuGlySerValLeuAsnAsn---AspThrValLeuCysValAspThrAlaGlu	291
Db	1237	GATGAGCCGAGATGGGTCTTGCAGAGGCCGAGGTTCTGAGCTCTGTGCACTGGAGCCAG	1296
Qy	292	LySGlnProProPheThrIleLeuArgSerLeuLeuArgValLeuLeuProGluSer	311
Db	1297	CCAGAGCGCGGGAGATGCATCTCTGGCGCAGTTTGGCTGGGAAAGAACTACTCTCCGAGGCA	1356
Qy	312	PheIleuIleValThrValArgAspValGlyThrGluValLeuValSerGlnValValSer	331
Db	1357	TCTCTTCTGATCAGAGGCTCGGACCCAGCAAGCTCTGCAGAAACTCATTTCTTTGGAGCAG	1416
Qy	332	ProArgGlyLeuLeuLeuValArgGlyTlSerGlyLeuGlnArgIleIleLeuLeuLeuGlu	351
Db	1417	GCAAGTGGGAGTGAAGGCTCTGGGGTCTCTGAGTCCAGACAGAAAGAAATATTTCTACAGA	1476
Qy	352	ArgGlyIleGlyGlnHisGlnIleThrGlnGlyLeuArgAlaIleMetAspAsnArgIleu	371
Db	1477	TATTTCAAGATGAAGGCAAGCAATTAAGACCTTTAGGTGGTGCATTAACAAGAAAG	1536
Qy	372	LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnIleu	391
Db	1537	CTCTGGGCGCTGTGTCTTGTGCTCGGAGGTGTCGTGGCTGGCTGCATGTGCTGATGCAG	1596
Qy	392	GlnAspValValGlyGlySerValAlaAspPheAsnGlnThrLeuThrGly-----Leu	409
Db	1597	CAGATGAAGCGGAAGAAAACTCACTGACTTCCAAAGCACAACAACCTCTGTCTA	1656
Qy	410	HisAlaIlePheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsn	429
Db	1657	CATTACTTCCCAAGCTCTCCAAAGCTCAGCAATTGGAA-----	1695
Qy	430	LeuGlnGluIleArgValValLeuValArgPheCysArgMetAlaValGlnGlyValThrAsn	449
Db	1696	-----CCCAAGTCAAGAGACTGCTGCTGCTGGCTGGCTGAGAGGAGATCTGGCA	1743
Qy	450	ArgIlySerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlySerGluLeu	469
Db	1744	AAAAAGACCTTTTCACTCAGACGACCTCAGAAAGATGGGTTAAGATGGGCGCATCTC	1803
Qy	470	ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspPheHisCysGlu	485
Db	1804	TCCACCTTCTGAAGATGGGTATTTCTTCAGAGCAACCCCACTCCCTCTGAGC-----	1854
Qy	486	GlnTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysValAlaIleTyrTyrVal	505
Db	1855	-----TAGCTTTCATTCACTCTGTGTTCCAAAGATTTCTTGCAGCAATGCTCTAATGTC	1908
Qy	506	LeuGlnLeuLeuGlu-----IleGlnProAlaLeuCysProLeuTyrValGlnGlyThr	523
Db	1909	TTGAGAGATGAGAGAGGAGGAGATGAACATCTTAATGATCATCAATGATTTGGAAAAGCG	1968
Qy	524	LyAspSerMetGluLeuValSerGlnAlaGlyPheHisIleHisSerLeuTrp-----	540
Db	1969	CTAGAGACA-----TATGAATACATGGCTGTGTGGGCGATCA	2007
Qy	541	MetValAspPheLeuPheGlyLeuValSerGlnAspValAlaArgAspProLeuGlnValLeu	560
Db	2008	ACCAACAGTTTCTAATTGGGCTGTTAAGTATGAGGAGGAGAGAGATGAGAAACATC	2067
Qy	561	LeuGlyCysProValProLeuGlyValIleGlnIleValLeuLeuHisThrIleValSerLeuLeu	580
Db	2068	TTTACATGTCGGCGCTGTCTCAGGG-----AGAAACTGAATGCACTGGTCCCTCCCTG	2121
Qy	581	Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrIleAspAlaPheHisCys	598
Db	2122	CAGCTGCTGCAGCGGCACAC-----TCTCGAGATGCTCTCACTGCG	2163



APPLICANT: Reed, John C.  
TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation  
FILE REFERENCE: P-LJ 3650  
CURRENT APPLICATION NUMBER: US/09/388,221B  
CURRENT FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 4200  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(4197)  
US-09-388-221B-3

Alignment Scores:  
Pred. No.: 1,83e-90 Length: 4200  
Score: 949.00 Matches: 387  
Percent Similarity: 35.79% Conservative: 190  
Best Local Similarity: 24.01% Mismatches: 458  
Query Match: 13.42% Indels: 579  
Gaps: 55

US-10-066-521-6 (1-1344) x US-09-388-221B-3 (1-4200)

QY 11 SerTyrglyLeuGlnTrpCysLeuTyrglyLeuAspTyrglyGlnPheGlnThrPhe 29  
DB 13 GCGTGGGGCCCGCTGACCTGTTACTGTGAGTTCCGAAAGAGAGAGCTGAGAGAGTTTC 72  
QY 30 LysGlnLeuLeuLysLysSerSerLysThrThrCysSerLysProGlnPhe 48  
DB 73 CAGCTTCGCTCGCCAAATMAAGCGCATCCAGAGCTTCGGGTGAGACACCGCTCAG 132  
QY 49 GlnIleGlnAAsnValGlnCysLeuAlaLeuLeuHisGlnTyrglyVal 68  
DB 133 CCAAGAAAGAGAGTGGCATGAGAGTGGCTGTAAGTGGTGGCTCAGTATGGGAG 189  
QY 69 SerLeuAlaTrpAlaThrSerLysSerLysPheGlnAAsnLeuArgThrLeuSer 88  
DB 190 CAGGGGGCTGGAGCTGACCTCATACCTGGAGAGAGATGGGGCTGAGGCTGACTGTC 249  
QY 89 GlnLysAlaArgAspAsp----- 94  
DB 250 GCCCAAGCCGAGAAAGGGGAGGCGCACTCTCTATTCCTTACAGCCCAAGTGAACCC 309  
QY 94 ----- 94  
DB 310 CACCTGGGGTCTCCAGCAACCACTTCACCGCATGCTAATGCTTGATCCATGAA 369  
QY 94 ----- 94  
DB 370 TTGGCGGGGGGTGACCCAGGGCTCAGAGAAAGGTTTGAAGACAGCTGCTGACACA 429  
QY 95 -----MetLysLysIleSerGlnAlaMet----- 102  
DB 430 TCTGAGCCGCTGAGAGAAATCTGCTCACTCTCTCAAGCTTCCAAAGCTCC 489  
QY 102 ----- 102  
DB 490 CCAAGCATGAGTCTCAAGCCAGAGATCCCAAGCCCAATCCACAGCAGAGTGTG 549  
QY 103 -----GlnGlnGlnGlyAla----- 107  
DB 550 GGGAGCTGGGAGTCCCACTCAAGCCAGCTGAGACCCAGAGAGAGAGGCTGCTGG 609  
QY 108 -----ThrAlaAlaGlnThrGlnGlu 114  
DB 610 ACCCAATGGCTCTGATGAACGTCAGAAATTTACTACAGAAATCAGAGAAAGAG 669  
QY 115 GlnGlnIleSerGlnAlaMetGlnGlnGlnGlnAlaThrAlaAlaGlnThrGlnGln 134  
DB 670 AGAGAGAAATCAGAGAAAGGAGAGCCCTCATGAGCGGTGTGAGAAAGCCCCCAAG 729

QY 135 GlyHisGlyGly----- 138  
DB 730 GCGCAGACCAAGCTTACAGCCCAACCAACCATGAGAGCTTCTGTGAGAGAGCCTC 789  
QY 139 ---AspThrTrpAspTyrglyLysSerHisValMetThr---LysPhe----- 151  
DB 790 TGTTCACATGGCCCTGGAAATATGAGAAATTTTACCAAAATTTCAACAGCTCTACTT 849  
QY 152 -----AlaGlnGlnLysAspValArgArgSerPheGlnAAsnThr 164  
DB 850 CTACAAAGACCTCAACCCAGAGCCAGAGATCCCTGCTCAAGAGAGC----- 897  
QY 165 AlaAlaAspTrpPro-----GluMetGlnThr 173  
DB 898 -----TGGCTGTATTATGTGAGAGAGATCGAGACATTTAATTGAGATCAGAGAC 948  
QY 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProAlaGlnValLeu 192  
DB 949 TTATTGGCCCAAGGCTGAGATACCAA-----GAACTCGCATGATCATCTG 996  
QY 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCystrPala 212  
DB 997 CAGGGGCTGCTGGAATTTGGAAAGTCAACATGSCCAGGAGAGAGTGAAGAGAGCTGGGG 1056  
QY 213 GlnGlyLysLeuTyrglnGlyMetPheSerTyrglyValPhePheLeuProValArgGluMet 232  
DB 1057 AGAGGCGAGCTGTATGGGAGACCGCTTCAGAGATCTTCTTCACTTCAGCTGAGAGACTG 1116  
QY 233 GlnArgLysLysGlnSerSerValThrGlnPheIleSerArgGlnTrpProAspSerGln 252  
DB 1117 GCCCAGTCCAAAGTGGTGAAGCTCTGAGAGTCAAGGAAAGTGGAGACACCACTCCG 1176  
QY 253 AlaProValThrGlnIleMetSerArgProGlnArgLeuPheIleAspGlyPhe 272  
DB 1177 GCTCCATTTAGACAGATCTGTCAGGAGAGGGGCTGCTTCACTTCAGTGAAGGTGA 1236  
QY 273 AspAspLeuGlySerValLeuAAsn---AspThrLysLeuCystrLysAspTrpAlaGln 291  
DB 1237 GATGAGCCAGAGATGGGCTTTCAGAGAGCCGAGTCTGAGCTGCTGCACTGAGAGCAG 1296  
QY 292 LysGlnProProMetThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSer 311  
DB 1297 CCACAGCCGGGAGTGAAGTCTGGGAGGTTGTGTGGGAAATCAATCTCCGAGAGCA 1356  
QY 312 PheLeuIleValThrValArgAspValGlyThrGlnLysLeuLysSerGlnValValSer 331  
DB 1357 TCTTCTGATGACAGGCTCGGACCAAGCTGTCAGAAACCTCATCTCTTGGAGCAG 1416  
QY 332 ProArgTyrglyLeuValArgGlyLysSerGlyGlnArgIleHisLeuLeuGln 351  
DB 1417 GCAGTGGGAGAGGCTCGGGGTCTGAGTCCAGAGAGAAAGAAATTTTCTACAGA 1476  
QY 352 ArgGlyIleGlyGlnHisGlnLysThrGlnGlyLeuArgAlaIleMetAAsnAspArgGlu 371  
DB 1477 TATTTCACAGATGAAGGCAAGCAATTAAGACCTTTAGGTTGGTCAATCAAAAGAG 1536  
QY 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391  
DB 1537 CTCTGGGCTGCTGTCTGTGGCTGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1596  
QY 392 GlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409  
DB 1597 CAGATGAAGCGGAGAGAAATCACTCACTGACTTCAAGACCAACCAACCTCTGCTGA 1656  
QY 410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValAlaArgArgCysLeuAAsn 429  
DB 1657 CATTAACCTTCCAGAGCTTCCAAAGCTCAAGCCATTGGGA----- 1695  
QY 430 LeuGlnGlnArgValValLeuLysArgPheCysArgMetAlaValGlnGlyValTrpAsn 449  
DB 1696 -----CCCAAGCTCAAGAGACTTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1743

QY 450 ArglySerValPheAspGlyAspAspMetValGlnGlyLeuSerGlyLeu 469  
 DB : : : : :  
 DB 1744 AAAAAGACCTTTTCAGTCCAGATGACCTCAGAAAGCATGGTTTATGATGGGCCATCATC 1803  
 QY 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu 485  
 DB : : : : :  
 DB 1804 TCCACCTTCTTGAAGATGGGTATCTTTCAGAGCACCCTCCCTCAGC----- 1854  
 QY 486 GluTyrTrpThrPhePheHisLeuSerLeuGlnAspPheCysAlaIleLeuTyrTrpVal 505  
 DB : : : : :  
 DB 1855 -----TACAGCTTCATTCACCTCTGTTTCCAAAGAGTCTTTGACGACATGCTTATGTC 1908  
 QY 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluLeuThr 523  
 DB : : : : :  
 DB 1909 TTGAGAGATGAGAAAGGGAGAGGTAAACATTTCAATCATCATATTTGGAAAGACG 1968  
 QY 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTyr----- 540  
 DB : : : : :  
 DB 1969 CTAGAGCA-----TATGGATATACATGGCCTTGTGGGGCATCA 2007  
 QY 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560  
 DB : : : : :  
 DB 2008 ACCACAGCTTTCATGAGGCTGTTAGTATGAGGGGAGAGAGACATGAGAAACATC 2067  
 QY 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuHisIleTrpValSerLeuLeu 580  
 DB : : : : :  
 DB 2068 TTTACCTGCGCGGTCTCAGGGG-----AGAACTCGATGACAGTGGTCCCGTCCCTG 2121  
 QY 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598  
 DB : : : : :  
 DB 2122 CAGCTGCTGTCAGCCACAC-----TCTCTGAGATCCCTCCACATGC 2163  
 QY 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618  
 DB : : : : :  
 DB 2164 TTGTACAGACTCCGAAACAAACGTTCTCTGACACAGTATGGCCCATTTGAAACAAATG 2223  
 QY 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638  
 DB : : : : :  
 DB 2224 GGCATGTGTGTAAGAAACAGACATGAGCTCTTAGTGTGACATTTCTGATTAATTCAGC 2283  
 QY 639 ProTyrLeuAspGlyValLeuArgValAspValLysGlyIlePheProArgAspGlnSerAla 658  
 DB : : : : :  
 DB 2284 CGCACAGTGAAGAGCTTCAGCTG-----ATTGAGGGC-----AGCACACACAGATCA 2331  
 QY 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGlnGlnIleTrp 678  
 DB : : : : :  
 DB 2332 ACATGAGGCCACCATGTGATCTCTGTTCAGTGGGTCCACATGACAGATGCCATTGG 2391  
 QY 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLysSer 698  
 DB : : : : :  
 DB 2391 ----- 2391  
 QY 699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718  
 DB : : : : :  
 DB 2391 ----- 2391  
 QY 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738  
 DB : : : : :  
 DB 2392 -----CAATTCCTCTTC 2403  
 QY 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeuLys 758  
 DB : : : : :  
 DB 2404 TCCGCTCTCAAGGTCAACGAACCTTAAGAGAGCTGAGCTTAAGTGAACCTCGCTGAGC 2463  
 QY 759 GluGluAspValArgMetAlaCysGlnAlaLeuLysHisProLysCysLeuLeuGluLys 778  
 DB : : : : :  
 DB 2464 CACTCTGACGTGAAGAGCTTTGTAAAGACCTGAGAGCCCTCGCTGCTCTGAGAGACC 2523  
 QY 779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrTrpLeuLysIleSerGlnIleLeu 798  
 DB : : : : :  
 DB 2524 CTGCGG----- 2529  
 QY 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValIleThrAspGlnGly 818

DB 2530 -----TTTTTTTTTTTGGCTGGC----- 2538  
 QY 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuLeu 838  
 DB : : : : :  
 DB 2538 ----- 2538  
 QY 839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858  
 DB : : : : :  
 DB 2539 -----TGTGCTTCACAGCTGAGAGCTGAGAGACCTTGGCTTTGGCTGAGAGCCAAC 2592  
 QY 859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeu 878  
 DB : : : : :  
 DB 2593 CAGACC----- 2598  
 QY 879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898  
 DB : : : : :  
 DB 2598 ----- 2598  
 QY 899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeu 918  
 DB : : : : :  
 DB 2599 -----CTG 2601  
 QY 919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlu 938  
 DB : : : : :  
 DB 2602 ACCGAGCTGACCTGAGCTTCATGTGCTCAGGATGCTGAGGCCAAACACCTTTGGCCAG 2661  
 QY 939 ValMetArgGluProSerCysHisLeuGlnAspLeuGlnLysValLysCysHisLeuThr 958  
 DB : : : : :  
 DB 2662 AGACTGAGACAGCCGAGCTGCAAGCTTACAGGAGCTGAGCTGTGTCAGCTGTGGCTTCAG 2721  
 QY 959 AlaAlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978  
 DB : : : : :  
 DB 2722 TCTGACTCTCCAGACCTGACCTGCTGTGCTTAGTGCACCCAGCTTAAGAGCTA 2781  
 QY 979 AspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnGlyLeuLys 998  
 DB : : : : :  
 DB 2782 GACCTGACAGAAACAACCTGATGACGTTGGCGGACATGCTGTGAGGGGCTCAGG 2841  
 QY 999 GlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCys-----Gly 1013  
 DB : : : : :  
 DB 2842 CATCTGCTCCCAATCTCATAGCTGCTGGGAAACCAATGTGATGACCCCTGAGAGGGC 2901  
 QY 1014 LeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArg----- 1030  
 DB : : : : :  
 DB 2902 CTG-----GATACGGAGAGATGATATGACATCTCTACCTCAAGCGGACAGACTC 2955  
 QY 1031 -----HisLeuThrSerLeuAsnLeu----- 1037  
 DB : : : : :  
 DB 2956 GGATCAGAGAGGGGGCTCCCATGTTGCTCAGGCTAATCTCAACTCTGAGCGTACG 3015  
 QY 1038 -----ValGlnAsnAsnPheSerProLysGlyMet-----MetLys 1049  
 DB : : : : :  
 DB 3016 AAGATCTTCCCAATGCTGATGATTCAGAGGAGAAAGCTCCCAAGAGGTGATCGGTGAA 3075  
 QY 1050 Leu-CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTr 1069  
 DB : : : : :  
 DB 3076 CTCTTGCGGTGCTCTCTCTGCTCTCAAGGGAGCTGCATAGAGAACCTTTGG----- 3130  
 QY 1069 PGIInTyrProValGlnIleArgLysLeuLeuGlnGluValGlnLeuLysProArgVal 1089  
 DB : : : : :  
 DB 3130 ----- 3130  
 QY 1089 IValIleAspGlySerTrpHisSerPheAspGluAspArgHisValLysIleGlyLeuThr 1109  
 DB : : : : :  
 DB 3131 -----GACTGTAC 3138  
 QY 1109 PheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuThrGlyMetAsnProGln 1129  
 DB : : : : :  
 DB 3139 GATGACTTTCGGGGCCCAAGGGGC-----CTGAGGCTACTGAGTACTT 3183  
 QY 1129 uGlnLysLysArgValSerLeuLeuAlaGlyAspPheLysSerThrArgPheAlaLys 1149

[illegible]

```

? RESULT 3
? US-09-388-221B-5
? Sequence 5, Application US/09388221B
? Patent No. 6818750
? GENERAL INFORMATION:
? APPLICANT: Reed, John C.
? TITLE OF INVENTION: No. 6818750e1 Card Proteins Involved in Cell Death Regulation
? FILE REFERENCE: P-LI 3650
? CURRENT APPLICATION NUMBER: US/09/388,221B
? CURRENT FILING DATE: 1999-09-01
? NUMBER OF SEQ ID NOS: 30
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 5
? LENGTH: 4332
? TYPE: DNA
?

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; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4332)
;
US-09-388-221B-5

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**Alignment Scores:**

Pred. No.:	1,94e-90	Length:	4333
Score:	949.00	Matches:	359
Percent Similarity:	36.80%	Conservative:	179
Best local Similarity:	24.56%	Mismatches:	423
Query Match:	13.42%	Indels:	502
DB:	4	Gaps:	49

US-10-066-521-6 (1-1344) X US-09-388-221B-5 (1-4332)

QY 11 SerTyrglyLeuGlnTrpCysLeuTyrglu--LeuAspIysGluGluPheGlnThrPhe 29

Db 13 GCCTGGGCGCCTGGCCTGTTACTTGAGTTCCTGAAGAAGAGGAGCTGAAGAGTTC 72

Qy 30 LysGluLeuLeuLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe 48

Db 73 CAGCTTCTGCTCGCCATAAGCGCACTCCAGGAGCTCTTCGGGTGAGACACCCGCTCAG 13

49 G N I L E G L I A A S N V A L G L u C y s l e u A l a l e u l e u l e u H I s G l u t y r i n g l y a l a 68

DB 133 CCAGAGAGACGAGTGGCAICGAGGTGGCCTCGTACCTGGTGGCTCAG---TATGGGAG 18

69 seLeUaIaIIPaIaInrserIeSerIePneGIuaBIweCaBILeuargInIleuSer 88

UD 130 CAGGCGCCCTGGACCTAACCCTCCTCAATACCTTGGAGGCAGAAAGGGCTAGAGGTCTACTTGATGCT 27

**xj**

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[illegible][illegible]

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430 TATTGGACGCGCTGGAGGAAATCTTCTGCGCTACCTTCCTCTACCAAGCTCTTCCAAAGCTCC 48

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QY 103 -----GlulGlulGlyAla--- 10

db 550 GGAGCTGGGATCCCCACCTCAGCCAGCCTAGCACCCAGAGAGCAGAGGCTCTGGG 60

Qy 108 -----ThrAlaAlaGluThrGluGlu 11

Db 610 ACCCAATGGCTCTTGATGAACGTCAGGAATTACTACACAGAAATCAGAGAAGAGAG 66

QY 115 GINGLIESERGINAmetGInglInglIyAlaThraIAAagluThrGIuglIn 13

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QY 135 GLYHISGLYGLY----- 13

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QY 139 ---AspThrTrpAspTyrLysSerHisValMetThr---LysPhe----- 15

Db 790 TGTTCACATGGCCCTGGAATAATGAGGATTTTAACCAAAATTCACACAGCTGCTACTT 84

QY 152 -----AlaGluGluGluAspValArgArgSerPheGluAsnThr 16

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Db      850 CTACAAAGACTCACCAGAGCAAGATCCCTGTCAGAGAGC----- 897
Qy      165 AlAlaAePTPro-----GluMeGlnThr 173
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Qy      174 LeuAlaGly--AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192
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Qy      193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCySTrpAla 212
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Qy      213 GlnGlyLeuLeuTyrglnGlnGlyMetPheSerTyrglyPhePheLeuProValArgGluMet 232
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Db      1237 GATAGCCAGAGATGGGTCTGTCCAGAGCCGAGTTCGAGTCTGTCTGCTGACCTGGACAG 1296
Qy      292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSer 311
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Qy      332 ProArgTyrglyLeuLeuValArgGlyIleSerGlyLeuGlnArgIleHisLeuLeuGlu 351
Db      1417 GCAGGTGGGTAGAGGCTCTGGGTTCTGAGTCCAGAGAAAGAAATATTTTACAGA 1476
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Qy      392 GlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409
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Qy      430 LeuGlnGluArgValValLeuLysArgPheCySArgMetAlaValGlnGlyValTrpAsn 449
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Qy      450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGlnLeu 469
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Qy      486 GlnTyrglyThrPhePheHisLeuSerLeuGlnAspPheCySAlaAlaLeuTyrglyVal 505

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Db      1855 -----TACAGCTTCATTACACCTGTGTTCCAGAGTTCTTTGACAGAACTCTATGTC 1908
Qy      506 LeuGlnGlyLeuGlu-----IleGluProAlaLeuCySProLeuTyrglyValGlnLysThr 523
Db      1909 TTGAGAGATGAAGAAAGGAGAGGTAAACATTTATATGATCACTAATGATTTGAAAGAGC 1968
Qy      524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleIleIleSerLeuTrp----- 540
Db      1969 CTAGAGCA-----TATGAATATACATGCGCTGTGTTGGGAGATCA 2007
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Db      2008 ACCACACGTTTCTTAATGGGCTGTTAAGTATAGAGGGAGAGAGAGATGAAGAACTC 2067
Qy      561 LeuGlyCySProValProLeuGlyValLysGlnLysLeuHisIleTrpValSerLeuLeu 580
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Qy      639 ProTyrglyLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGlnSerAla 658
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Db      2332 ACATGAGCCCAACCATGATGTGCTGTCGAGTGGGTCGACAGAGCAAGATGCTATTTG 2391
Qy      679 GluAspPheCySserMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698
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Qy      759 GlnGluAspValArgMetAlaCySGlnAlaLeuLysHisProLysCySLeuLeuGlnLys 778
Db      2464 CACTCTGAGATGAAGAGCTTTGTAAAGCCTTGAGAGCCCTTGGCTGCTCTGAGAGCC 2523
Qy      779 LeuArgLeuAspCySArgLysLeuThrHisAlaCySArgLysLeuLysIleSerGlnIleLeu 798
Db      2524 CTGGCG----- 2529
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Db      2530 -----TGGCTGCTGC----- 2538
Qy      819 ValMetProLeuSerAspAlaLeuArgValSerGlnCySAlaLeuGlnLysLeuIleLeu 838
Db      2538 ----- 2538
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QY 919 ThrHisLeuSerLeuSerMetAsnProValGlnAspAsnGlyValAlaLeuLeuCyAsnGlu 938
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Db 2902 CTG-----GATACGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2955
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Db 2956 GGATCAGAGAGAGGGGCTTCCCATGTTGCTCAGGCTGATTCCAACCTCTGACGTGAC 3015
QY 1038 -----ValGlnAsnAsnPheSerProLysGlyMet--MetLys 1049
Db 3016 AAGATCTTCCCAATGTGATGATTCAGAGAGAAAGCTCCCAAGAGTGTACCGGTGAA 3075
QY 1050 Leu-CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeuTrpLysTr 1069
Db 3076 CTCTGTGCGGTGCTTCTCTGCTCTGCTCAAGGGAGCTGCAATGAGAGCTTTGG----- 3130
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QY 1109 PheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProG 1129
Db 3139 GATGACTTCTGGGGCCCGACGGGC-----CTGTGGCTACTGAGTACTT 3183
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Db 3215 -TCCCTGAGCTGCTCTTACCGCTGCGCCAAAC--CGGCTCTCTGCTGTGATGAGA 3270
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QY 1189 --TyrSerGlyAlaTrpSerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAla 1208
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Db 3418 GTGGCTCTCCAAAGGG--GCCATGTGACATCCCTGT--TCCAAATGGCCCACTTTAA 3473
QY 1246 LysSerArgGly-----TrpCysLeuAsnSerAlaAspArgHisSerGlyValSerTrp 1264
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QY 1264 er 1264
Db 3513 GC 3514

RESULT 4
US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4272)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-388-221B-11

Alignment Scores:
Pred. No.: 2,646-90 Length: 4466
Score: 948.00 Matches: 360
Percent Similarity: 38.47% Conservative: 207
Best Local Similarity: 24.42% Mismatch: 529
Query Match: 13.40% Indels: 380
DB: 4 Gaps: 46

US-10-066-521-6 (1-1344) x US-09-388-221B-11 (1-4466)
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QY 30 LysGluLeuLeuLysLysSer---SerGluSerThrThrCysSerLleProGlnPhe 48
Db 73 CAGCTTCTGCTCGCAATTAAGCGCACTCCAGAGGCTTCTGGGTGAGACACCTGCTCAG 132
QY 49 GluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGlyTyrglyVala 68
Db 133 CCAGAGAAAGAGAGTGCATGAGAGTGGCTCTGACTGTGGTGCAG--TATGGGAG 189
QY 69 SerLeuAlaTrpAlaTrpSerLleSerLlePheGluAsnMetLeuAsnArgThrLeuSer 88
Db 190 CAGCGGCTCGAGACTGACCTCATATCTGGAGGAGATGGGGCTGAGGTCACTGTC 249
QY 89 GlnLysAlaArgAspAp----- 94
Db 250 GCCCAAGCCAGAGAGGGGAGGCGCACTTCCCTCATTTCCCTTACAGCCCAAGTGAACCC 309
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QY 94 ----- 94  
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QY 95 -----MetLysLysIleSerGlnAlaMet----- 102  
Db 430 TCTGAGCGCCGTGAGAGAAATCTGCTCACTCTCACTCAAGCTTTCAGAGCTCC 489  
QY 102 ----- 102  
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QY 103 -----GluGlnGluGlyAla--- 107  
Db 550 GGGAGCTGGGGATCCCACTCAGGCCAGCTAGACCCAGAGAGAGAGGCTCTGG 609  
QY 108 -----ThrAlaAlaGluThrGlu 114  
Db 610 ACCCAATGCTCTGATGAACGTCAAGAAATTACTACAGAAATCAGAGAAAGAG 669  
QY 115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGln 134  
Db 670 AGAGAGAAATCAGAGAAAGCAGAGCCCATGGGAGCGGTGATGAAACCCCCACAG 729  
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Db 1744 AAAAAGACCTTTCACTCAGATGACCTCAGAAAGATGGGTTAAGTGGGGCATCATC 1803  
QY 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCyseGlu 485  
Db 1804 TCCACCTTCTTGAAGATGGGATATCTTCAAGAGCAACCCATCCCTGAGC----- 1854  
QY 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCyseAlaAlaLeuTyrTyrVal 505  
Db 1855 -----TACAGCTTCACTCACTCTGTTCGAAAGTCTTTCGAGCAATGCTCATGTC 1908  
QY 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCyseProLeuTyrValGluLysThr 523  
Db 1909 TTGAGGATGAGAGGGGAGAGGTAAACATCTTAATGATCATATGATTTGGAAAGAGC 1968  
QY 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540  
Db 1969 CTAGAGACA-----TATGAATACATGGCTGTGTGGGGCATCA 2007  
QY 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValAlaArgArgProLeuGluValLeu 560  
Db 2008 ACCACAGCTTCTTAATGGGCTGTATAGTATGAGGGGAGAGAGATGAGAAATC 2067  
QY 561 LeuGlyCyseProValProLeuGlyValLysGlnLysLeuHisIleTrpValSerLeuLeu 580  
Db 2068 TTTCACTGCGGCGGTGTCAAGGG-----AGAAACGTGAGAGAGTGGTCCCGTCCCTG 2121  
QY 581 Gly-----GlnGlnProAsnAlaThrThrProGluAspThrLeuAspAlaPheHisCyse 598  
Db 2122 CAGCTGCTGTGCGCACAC-----TCTGTGAGTCCCTCGACCTG 2163  
QY 599 LeuPheGluThrGlnAspValGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618  
Db 2164 TTGTACGAGCTCGGAACAAACGTTCTCTGACACAGATGAGCCCATTTGGAGAAATG 2223  
QY 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCyseLeuGlnHisCyse 638  
Db 2224 GGCAATGTGTAGAAACAGACATGAGCTTTAATGTGCACTTCTGATTAATTCAGC 2283  
QY 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAla 658  
Db 2284 CGCCAGGTGAAGAGCTTCAAGCTG---ATTAGAGC-----AGCCAGACACAGATCA 2331  
QY 659 GluAlaCyseProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrp 678





QY 486 GluTyrThrPhePheHisLeuSerLeuGlnAspPheCysValAlaLeuTyrTyrVal 505  
D 1855 -----TACAGCTTCATTCACCTCTGTTCACAGAGCTTCCTTGAGCAAGATCTCATATGTC 1908  
QY 506 LeuGluGluLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluGluPhe 523  
D 1909 TTGGAGGATGAGAAAGGAGAGGATTAACATTCATTAATGCATTAATGATTTGGAAAGACG 1968  
QY 524 LysArgSerMetGluLeuGluGlnAlaGluPheHisIleHisSerLeuTyr----- 540  
D 1969 CTAAAGAG-----TATGGAATACATGGCTCTTGGGGGACATCA 2007  
QY 541 MetLysArgPheLeuPheGluLeuValSerGluAspValArgArgProLeuGluValLeu 560  
D 2008 ACCACAGCTTCCTATTTGGGCTGTTAAGTATGATGAGGGGAGAGAGATGAGAAACATC 2067  
QY 561 LeuGluCysProValProLeuGluValLysGlnLysLeuHisIleTyrValSerLeuLeu 580  
D 2068 TTTCACCTGCGGCTGTCAAGGG-----AGAACTGATGCAAGTGGGTCCTGCTCCCTG 2121  
QY 581 Gly-----GlnGlnProAsnAlaThrThrProGluAspThrLeuAspAlaPheHisCys 598  
D 2122 CAGCTGCTGCTGCAGCCACAC-----TCTCTGAGTCCCTCCATCTGC 2163  
QY 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618  
D 2164 TTGTACAGACTCCGAAACAAACGTTCTTGACACACAGTATGAGCCCATTTGGAAAGATG 2223  
QY 619 ThrLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638  
D 2224 GGCATGGTGATGAACACAGATGAGCTTTAGTGTGCACCTTCTGATTAATATTCAGC 2283  
QY 639 ProTyrLeuArgLysIleArgValAspValLysGluIlePheProArgAspGluSerAla 658  
D 2284 CGCCACGTGAAGAGCTTCAGCTG---ATTGAGGGC-----AGCAGACAGATCA 2331  
QY 659 GlnAlaCysProValValProLeuTyrMetArgAspLysThrLeuIleGluGlnGln 678  
D 2332 ACATGAGACCCACCATGATGATGCTGTTCAGTGGGTCACAGTACAGATGCTATTTGG 2391  
QY 679 GluAspPheCysSerMetLeuGluYThrHisProHisIleuArgLysLeuAspLeuGlySer 698  
D 2391 ----- 2391  
QY 699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718  
D 2391 ----- 2391  
QY 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGluValGlnHisLeuTyr 738  
D 2392 -----CAGATTCTCTTC 2403  
QY 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGluYThrHisIleuLys 758  
D 2404 TCCCTCTTCAGAGTCCACCAAGAACCTGAAGAGCTGAGCCTTAATGTGAAGAACTCCGTAAGC 2463  
QY 759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSer 778  
D 2464 CACTCTGCAAGTGAAGAGCTTTGTAAAGCTTGAAGCCCTGCTGCTGCTCTGAGAAC 2523  
QY 779 LeuArgLeuAspCysCysGluLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeu 798  
D 2524 CTGGGTTGGCTGCTGCTGCTGCTCAGCTGAGAGCTGCAAGACCTTGGCTTTGGGCTG 2583  
QY 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGluLysValThrAspGlnGly 818  
D 2584 AGAGCCACAGACCTTGAAGCTGAGCCTGAGCTTCATTAATGCTCAACGAGAGCTTGA 2643  
QY 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838  
D 2644 GCCAAACACTTTTGCAGAGACTAGACAGCCGAGCTGCAGAGCTACAGAGCTGAGCTG 2703

QY 839 GluAspCysGluYIleThrAlaThrGluCysGlnSerLeuAlaSerAlaLeuValSerAsn 858  
D 2704 GTACGCTGTGGCTCAGAGCTGAGCTGCTGCAGAGACCTGGGCTGTGGTATGAGTCAAGC 2763  
QY 859 ArgSerLeuThrHisIleuCysLeuSerAsnAspSerLeuGluLysGlnGluValAspLeu 878  
D 2764 CCCAGCTTGAAGAGCTTAAGACTTCCAGACAGAACCTGGATGACGTTGGGCTGCGACTG 2823  
QY 879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898  
D 2824 CTCTGAGAGGGCTCAGAGCATCTGCTCGAAATCATTAAGCCCTGGGGCTGACAGACCA 2883  
QY 899 HisLeuAsp----- 901  
D 2884 ACTGTAGTATGATGATGAGGACAGAACTGAGGCTCGAGACAGAAACCTCAGCTG 2943  
QY 902 -----ThrAlaGluCysGluPheLeu 908  
D 2944 CTCACTTTCAGACAGAGAAACCAAGTGTATGACCCCTACTGAGGGC-----CTG 2994  
QY 909 AlaLeuAlaLeuMetGluAsnSerTyr-----LeuThrHisIleuSerLeu----- 923  
D 2995 GATACGGGAGAGATGAATATAGCAATCTCACTCAAGGGGACAGAGCTCGATCAAG 3054  
QY 924 ---SerMetAsnProValGluAspArgGluValLysLeuLeu----- 936  
D 3055 AGGGCGCTTCCCAATGTGTCTCAGGCTTAATCTCAAACTCTCGAGCCTGAGCAAGATCTTC 3114  
QY 937 -----CysGluValMetArgGluProSerCysHisIleuGlnAspLeuGluVal-Lys 954  
D 3115 CCAATTCGTAGATTCGACAGAGAAAGCTCCCAAGAGTATGACCGGTGGAACTTTGGC 3174  
QY 954 sCys-----HisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArg 971  
D 3175 GTGCTTCTCTGCTGCTCAAGGGAGCTGATATGAAAGCTTTGGGAGCTGAGATGAC 3234  
QY 971 gSerArgHisIleuLysSerLeuAspLeu-----ThrAspArg 983  
D 3235 TTTCGTGGGCTTGAAGAAATGTGATGTGATGATTAAGACACAAACAGATAC 3294  
QY 983 nAlaLeuGluLysAspLysValAlaAlaLeuCysGlu----- 995  
D 3295 AGCGTTGGTTCCTCCCACTGCTGCTGCTGTGTGTGTGTCAGACAGAGCTCGGCTTCTG 3354  
QY 996 -----GlyLeuLysGlnLysAsnSerValLeuThrArgLeuGluLysValaCysGluLe 1014  
D 3355 GTAAGGATAGAGTCAAGATGAGATGCGTTGTGCTTCGAGTCAAGACCTGCGCTG 3414  
QY 1014 uThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArgHisIleuThrSe 1034  
D 3415 GACCTGACAGACCATGAACAGTGGCTGTGGGCGGCCCTTGTGTGATGTCACTGACAGAG 3474  
QY 1034 rLeuAsnLeuValGlnAsnAsnPheSerProLysGluMetMetLysLeuCysSer----- 1052  
D 3475 C-----CAGAGAGAGCTGTGCGGAAATCCACCTCCCACTTCATCTCCCTC 3522  
QY 1053 -----AlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu-----TyrLys 1068  
D 3523 CAAGCTGAGGTGAGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3582  
QY 1068 sTyrGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLysProArg 1088  
D 3583 CTGGAG-CATCCAGCCCGGGGTGAGCTTTCATATGCTGTCTCGA-----ACCCCCAG 3635  
QY 1088 gValValIleAspGlySerTyrHisSerPheAspGluAspArgHisIleLysIleGlyLe 1108  
D 3636 CTTCCTCTGATGTGGCATCTCTGCTGAGATGCGCAGTGGAGCTGCTTCACATCCCAT 3695  
QY 1108 uThrPheArgLeuProLysSerArgAlaTyrProCysAlaLeuLeuTyrGluMetAsnPr 1128  
D 3696 CACTTCCAC-----ACATTGATCATTAATACCCCCACCC 3731  
QY 1128 oGluGln---LysLysArgValSerLeuLeuAlaGluAspPheLysSerSerThrArgPh 1147

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Db 3732 CGAAGATATTAAGTTCACCTTGTACCTTGCCCGACGAC----- 3771
Qy 1147 eAlaLysSerLeuCySLeuAlaThrAlaSerGlyLeuSerGlnArgValaAspAlaGly 1167
Db 3772 -----GCCTTGCTTAACAAAGCGATAGATGATGAAGATCGCTTCATGATGTCG 3824
Qy 1167 uGlnSerSerProGlnProMetAla-----GlyThrGlnHis----- 1179
Db 3825 CCGGAGACTTCGCCCCCAATGGAACCCCTGAACCTTGCTTCATGATGATGTCGTA 3864
Qy 1180 -----LysGlnAspLysMet----- 1184
Db 3885 TTCTGCTAACCTGAAGATATGCCCAAGAGATGTAATGTCCTACAGAGCCCTGAGAGA 3944
Qy 1185 -----LeuSerValGlyTyrSerGlyAlaThrSerGlnThrAlaGluLeuGlu 1201
Db 3945 AATTCAGACATTCCTCAAAATTCATATGCTGGCGAGATGGAAGAACCATTCAGAG-- 4002
Qy 1201 yLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaThrSerLeuGlyArgGly 1221
Db 4003 -----ATTACTGAAAAAGACATGGAGCTTGGTGGGATCTGA-GGTGA 4048
Qy 1221 uLeuSerSerArgGlyLeuCyS-----ProThrValLeuMetThrThrAlaVal 1237
Db 4049 AGCCAGTGAATCTCAGCTTGTAGCTGATCAGCCCTCCTCTTCAGGTGACGCT 4108
Qy 1237 lCySProGly 1240
Db 4109 TTGTGAAGGA 4118

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## RESULT 6

```

US-08-910-731-3
Sequence 3, Application US/08910731
Patent No. 5932440

```

## GENERAL INFORMATION:

```

APPLICANT: CHATTERJEE, DEB K.

```

```

TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof

```

```

NUMBER OF SEQUENCES: 16

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

```

```

STREET: 1100 NEW YORK AVE., N.W., SUITE 600

```

```

CITY: WASHINGTON

```

```

STATE: D.C.

```

```

COUNTRY: USA

```

```

ZIP: 20005-3934

```

```

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk

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OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: Patentin Release #1.0, Version #1.30

```

```

CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/910,731

```

```

FILING DATE: (Herewith)

```

```

CLASSIFICATION: 435

```

```

PRIORITY APPLICATION DATA:

```

```

APPLICATION NUMBER: 08/795,395

```

```

FILING DATE: 04-FEB-1997

```

```

PRIORITY APPLICATION DATA:

```

```

APPLICATION NUMBER: 08/794,546

```

```

FILING DATE: 03-FEB-1997

```

```

PRIORITY APPLICATION DATA:

```

```

APPLICATION NUMBER: 60/024,057

```

```

FILING DATE: 16-AUG-1996

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: ESMOND, ROBERT W.

```

```

REGISTRATION NUMBER: 32,893

```

```

REFERENCE/DOCKET NUMBER: 0942.3440003

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: 202-371-2540

```

```

TELEFAX: 202-371-2540

```

```

INFORMATION FOR SEQ ID NO: 3:

```

```

SEQUENCE CHARACTERISTICS:
LENGTH: 1374 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-910-731-3

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## Alignment Scores:

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Pred. No.: 4,28e-57 Length: 1374
Score: 630.50 Matches: 151
Percent Similarity: 51.38% Conservative: 73
Best Local Similarity: 34.63% Mismatches: 205
Query Match: 8,91# Gaps: 3
DB: 2

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US-10-066-521-6 (1-1344) x US-08-910-731-3 (1-1374)

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Qy 653 ProArgAspGluSerAlaGluAlaCySProValProLeuThrMetArg-----Asp 670
Db 39 CGGTGACAGAGCTCTCCCTGATCCAACATACCAAG-TGGTC-AGGCTGATGAC 96
Qy 671 LysThrLeuIleGluGluGlnThrProGluAspPheCysSerMetLeuGlyThrHisProHis 690
Db 97 TGTGGCTCACTGAAGTGGGCGGAGCAAGATCCAGAGTCAAGGATCAGGACCCACTGCC 156
Qy 691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLeuThrLeuCyS 710
Db 157 CTGACAGAGCTCAGCTATGACCAATGATGAGTGGGTATGCTGGTGGTGGTGGTGGTGGTGC 216
Qy 711 AlaLeuLeuArgHisProThrCySLeuIleGlnThrLeuMetPheArgAspAlaGlnIle 730
Db 217 CAGGCTCAGCAATCCCACTTGTAAGATCCAGAAAGCTGACGCTTCAAGAACTGACGCTTG 276
Qy 731 Thr---ProGlyValGlnHisLeuThrArgIleValMetAlaAsnArgAsnLysSer 749
Db 277 AGGAGAGCTGGCTGGGGGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGAA 336
Qy 750 LeuAsnLeuGlyIleThrHisLeuLeuGluGluAspValArgMetAlaCySAlaLeuLeu 769
Db 337 CTACATCTCATGACAAACCTCTGGGGGATGAAAGGCTGAAGCTGCTGTAAGAGGATC 396
Qy 770 LysHisProLysCySLeuLeuGluSerLeuArgLeuAspCySArgLeuThrHisAla 789
Db 397 CGGAGCCCGCAGTCCGCTGAGAAAGCTTCAAGTGAATCTGAACCTGACAGCTGACC 456
Qy 790 CysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSer 809
Db 457 AGCTGCGAGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516
Qy 810 AlaGlyAsnLysValThrAspGlyValMetProLeuSerAspAlaLeuArgValSer 829
Db 517 AGCAACATGACTTCATGAGGCTGGTATCCACACTCTGTGCCAGGCTGAAGATTC 576
Qy 830 GlnCySAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCySAla 849
Db 577 GCTGTCAATCGAGTCACTCAAACTGGAAGCTGTGATCACTCAAGCACTGCAAG 636
Qy 850 SerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCySLeuSerAsn 869
Db 637 GATCTGTGATGTGGTGGCTTCAAAAGCTTCACTGCAAGAACTGAACTGAACTGAACTGAA 696
Qy 870 SerLeuGlyAsnGluGlyValAsnLeuLeuCySArgSerMetCysLeuProHisCysSer 889
Db 697 AAGCTGGCAACACAGGATTCAGACACTGTGCTCAGAGCTGCTTCCAGCTGACG 756
Qy 890 LeuGlnArgLeuMetLeuAsnGlnCySHisLeuAspThrAlaGlyCySArgPheLeuAla 909
Db 757 CTGAGAGACTGTGGCTGCTGAGACTGATGTCACTGCAAGAGCTGCAAGAACTGCTGTC 816

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Qy 910 LeuAlaIeuMeCgIyAenSerTrrpleuThrhIleuSerIeuSerMetAenProValGlu 929  
Db 817 CGTGTCTCAGAGCCAGACAGAGCTGAGAGAACTCAGCTTACCTGAGCAAGCTGAG 876  
Qy 930 AspAengIyValIyIeuIeuCyGgIyValIeuMetAArgIyProSerCyGhiIleuGlnAsp 949  
Db 877 GATGAGGTGGCCCAACTCTGTGTGAAGAGCTGTGAAGAGCTGTGAGCTGTGAGCTGAGCA 936  
Qy 950 LeuGluIeuValIyIeuCyGhiIleuThraIAlaIyCyGgIySerIeuSerCyValIle 969  
Db 937 CTGTGGGTAAGACCTGTAGCTCAGAGCTGCTGTCTGCCCACTTCTGCTCGGTGTG 996  
Qy 970 SerArgSerArgIhIleuIySerIeuAspIeuThraIAspAlaIeuGlyIy 989  
Db 997 ACCAAAACAGCTTCTCTGTGTGAAGTGCATGCAATGAGCAACCCGCTGGAGACTCGGGA 1056  
Qy 990 ValAlaIeuIeuCyGgIyIyIeuIySerIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 1009  
Db 1057 GTCTGGAGCTTTGCAAGCCCTGGGGCTATCCGACACAGATGCTGCTGTGCTGTG 1116  
Qy 1010 LysAlaIyGgIyIeuThrSerAspCyGgIyAlaIeuSerIeuAlaIeuSerCyAsn 1029  
Db 1117 GGAGACTGTGATGTGACAGACAGTGTGCTGACAGCTTGCACCTGCTGTGCTGAGCAAC 1176  
Qy 1030 ArgIhIleuThrSerIeuAspIeuValGlnAspIeuSerProIyGlyMetMetIy 1049  
Db 1177 CGCAGCTTGAGGAACTGCACTCAATGCACTGCAATGAGGAGCAACAGGCTGCTCA 1236  
Qy 1050 LeuCySerAlaIeuIy 1066  
Db 1237 CTGCTGAGAGCTTCAACAGCCCACTGCACTGCTGCACTGCTGCTGCTGCTGCTG 1236  
Qy 1067 ---TrrIy 1081  
Db 1297 TACTGAGAGATGAGTGAAGACCAAGCTTGGGGCTGAGAGAGAA 1344

RESULT 7  
US-08-795-395-3  
Sequence 3, Application US/08795395  
Patent No. 5965399  
GENERAL INFORMATION:  
APPLICANT: CHATTERJEE, DEB K.  
TITLE OF INVENTION: Cloning and Expression of Rat Liver and  
NUMBER OF INVENTION: Porcine Liver Ribonuclease Inhibitor  
CORRESPONDENCE ADDRESS:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVE., N.W., SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,395  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/024,057  
FILING DATE: 16-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ESMOND, ROBERT W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0942.3440002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1374 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
NAME/KEY: CDS  
LOCATION: 1..1368  
US-08-795-395-3

Alignment Scores:  
Pred. No.: 4.28e-57 Length: 1374  
Score: 630.50 Matches: 151  
Percent Similarity: 51.38% Conservative: 73  
Best Local Similarity: 34.63% Mismatches: 205  
Query Match: 8.91% Indels: 9  
DB: 2 Gaps: 3

US-10-066-521-6 (1-1344) x US-08-795-395-3 (1-1374)

Qy 653 ProArgAspGluSerAlaGluAlaCyProValIyProIeuThrMetArg-----Asp 670  
Db 39 CCGGTGACAGAGAGTCTTCCCTGATCCCAACATACCAAG-TGGTC-AGGCTGAGTAC 96  
Qy 671 LysThrIleuIleuGluGlnIy 690  
Db 97 TGTGGCTCACTGAAGTGGGTCGCAAGACATCAAGTCAAGATCCAGGACCCAGCCCTGCC 156  
Qy 691 LeuArgGluIeuAspIeuIyIySerIleuThrGluArgIleuIyIyIyIyIyIyIyIyIy 710  
Db 157 CTGACAGAGCTCAGCTTACGCAACCAATGAACTGGATGATGCTGTGGGTGTGCTC 216  
Qy 711 AlaIyIeuArgIhIyProIy 730  
Db 217 CAGGGCTGAGAGATCCCACTTGAATCCAGAGAGTGAAGCTTCAAGACTGACGCTG 276  
Qy 731 Thr--ProGlyValGlnIleuIy 749  
Db 277 ACGGAGCTGCTGTGGGTCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 336  
Qy 750 LeuAspIeuGlyIy 769  
Db 337 CTACATCTCAATGACCAACCTTGGGGAGTGAAGCTGCAAGCTGCTGTGAAGACT 396  
Qy 770 LysIhIyProIy 789  
Db 397 CGGAGCCCAAGTCCCTGTGAGAACCTTCAAGTGAATATCTTAACCTCACAGCTAAC 456  
Qy 790 CyIy 809  
Db 457 AGCTGAGCCCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516  
Qy 810 AlaGlyIeuIyValIy 829  
Db 517 AGCAACATGATCTTCATGAGGCTGTATCCACTGTGTGCCAGGCTGGAAGATCT 576  
Qy 830 GlnCyAlaIeuGluIy 849  
Db 577 GCTGTCACTGAGTCACTCAACTGAGAACTGTGTATCACTTAAGCACTGCAAG 636  
Qy 850 SerIeuIy 869  
Db 637 GATCTGTGATGTGTGGCTCCAAAGCTCACTGCAAGAACTGAGCTGGAGCAAC 696  
Qy 870 SerIeuIy 889  
Db 697 AAGCTGGCAACACAGGATGCAAGCTGTGTCAAGAGCTGCTGTCCAGCTGAG 756  
Qy 890 LeuGlnArgIeuIy 909  
Db 757 CTAGAGACTGTGGCTTGGAGCTGTATGTCTCAAGAGGCTCAAGAGACTGTGC 816



Oy		910	leu1alaMetGlyAuaSerTrpLeuThrHnHisLeuSerLeuSerMetAspProValIgu	929
Dd		817	CGTCTCTCCAGACGCCAACAGACCTTGAAGAATCAGCTCAAGCTGGCGAAATGACTGAAG	876
Oy		930	AAPhaNGlYAlaLYLeuLeuCysGlUValMetArgLUpProSerCysHISLeuGIlnaP	949
Dd		877	GATGAGGGTGCCCAACTGTCTGTGTGAAGACCTTTGAAGACCTGGGTGTCACTGGACATCA	936
Oy		950	LeuGIlnaValLYsCysHISLeuThrLaalaaCYsCySGluSerLeuSerCYeValIlle	969
Dd		937	CTGTGGCGTAAGAAGACCTGTAAAGCTCAACAAGCTGCCTTGTCCCACTTCGTGCGGTGTG	996
Oy		970	SerArgSerArgHISLeuLYSLeuSerLeuaspLeuThrAspAmnalaleuGLYAspGLYLyl	989
Dd		997	ACCAAATAACAGTCTCTGTTTGAGTTCGAAATAGACAAACCCGCTGGAGACTCCGGGA	1056
Oy		990	ValAlaalalaLeuCYsGluGlyLYleuLYsglinLYsaMSerValLeuThrArgLeuGLYleu	1009
Dd		1057	GTCTGTGAGCTTTGTGAAGAGCCCTGGCGCTATCCGACACAGTGCCTGCTGCTTTGGCTG	1116
Oy		1010	LYsaLaCYsGlyLeuThrSerAspCYsCySGluAlaleuSerLeuAlaleuSerCYasAn	1029
Dd		1117	GGAAGACTGTATGTACACAGACAGTGGCTGCAGACACCTTGGCACATGCTCTGTGGCCAAAC	1176
Oy		1030	ArgHISLeuThrSerLeuasnLeuValGIlnanbspHeSerProLYsglyMetMetLYs	1049
Dd		1177	CGCAGCTTGAAGGAACGTGAAGCTCAGTAAACAATGCAATGGAGGGAGCAACAGGTGTCTTAACA	1236
Oy		1050	LeuCYsSerAlaPheAlaCYsProThrSerAsnLeuGlnlleilegLYleu-----	1066
Dd		1237	CTGTCTGAGAGCCTTCAACACAGCCGACGTCAATCTTCAAGCAGCTTGTCTGTATGACATT	1236
Oy		1067	---TrpLYstrpGlnTYrProValGIlnleArgLYsLeuLeuGluGln	1081
Dd		1297	TACTGACGATGATGAGTGAAGACAGGCTTGCGGGCTTGAAGAGAGAA	1344

RESULT 8  
 US-08-910-731-1  
 Sequence 1, Application US/08910731  
 Patent No. 5932440  
 GENERAL INFORMATION:  
 APPLICANT: CHATTERJEE, DEB K.  
 APPLICANT: SHANDILYA, HARINI  
 TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVE., N.W., SUITE 600  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,731  
 FILING DATE: (herewith)  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/795,395  
 FILING DATE: 04-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/794,546  
 FILING DATE: 03-FEB-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/024,057  
 FILING DATE: 16-AUG-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ESKMOND, ROBERT W.  
 REGISTRATION NUMBER: 32,893

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REFERENCE/DOCKET NUMBER: 0942.3440003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-910-731-1

Alignment Scores:
Pred. No.: 4.49e-56 length: 1371
Score: 621.00 matches: 151
Percent Similarity: 50.11% conservative: 86
Best Local Similarity: 31.92% mismatches: 210
Query Match: 8.78% indels: 26
DB: 2 gaps: 5
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QY 645 ArgValaAspValLysGlyIlePheProArgaAspGluSerAlaGluAlaCybProValVal 664
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QY 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleYthrHisLeuLysGlu 759
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QY 780 ArgLeuAspCybCybGlyLeuThrHisAlaCybTyrLeuLysIleSerGlnIleLeuThr 799
DB 427 CAGTGGAGTACTGCGCGCTGACGCGCGCTGACCTGAGACCCCTGCGCTGCTCAGG 486
QY 800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
DB 487 GCCACGCGGCGCTTAAAGAGCTCAGCGTGAACAACAAGACATCGGCGAGCGCGGCC 546
QY 820 MetProLeuSerAspAlaLeuArgValSerGlnCybAlaLeuGlnLysLeuIleGlu 839
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QY 840 AspCybGlyIleThrAlaThrGlyCybGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
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Qy 860 SerLeuThriHisLeuCyValLeuSerAsnAsnSerLeuGlyAsnGlyValAsnLeuLeu 879
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Qy 880 CysArgSerMetAlaGlyLeuProHisCySerLeuGlnAlaGlyLeuMetLeuAsnGlnCysHis 899
Db 727 TGCCTCCGGGCTCTTGAAGCCCGCTCCCGCTCAAGACCTGTGTGCTGTGGAGAGTGTAC 786
Qy 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThr 919
Db 787 ATCAGCGCAGTGTGTGAGAGAGACTTGTGCGGTGCTTCCAGGCGCAAGAACCTGTAG 846
Qy 920 HisLeuSerLeuSerMetAsnProValGlnAspAsnGlyValAlaLeuLeuCySerGlyVal 939
Db 847 GAGCTCACTGTGGCGGAGCAACAGCTGGGCGCAGAGGGCGCCGGCTGCTGTGCGAGAGC 906
Qy 940 MetArgGluProSerCysHisLeuGlnAspLeuGluValValCysHisLeuThrAla 959
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Qy 1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
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Qy 1040 AsnAsnPheSerProGlyGlyMetMetLeuLeuCySerAlaPheAlaCysProThrSer 1059
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Db 1267 GCCCTGGGAGCACTGTGCTGTGACGACCTTACGAGCAGGAGGAGTGAAGAGACCGGCTGC 1326
Qy 1080 GluGluValGlnLeuLeuLysPro-----ArgValVal 1090
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RESULT 9  
 US-08-795-395-1  
 ; Sequence 1, Application US/08795395  
 ; Patent No. 5965399  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHATTERJEE, DEB K.  
 ; APPLICANT: SHANDILYA, HARINI  
 ; TITLE OF INVENTION: Cloning and Expression of Rat Liver and  
 ; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
 ; STREET: 1100 NEW YORK AVE., N.W., SUITE 600  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/795,395

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; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FRAGMENT:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-795-395-1

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Alignment Scores:  
 Pred. No.: 4,49e-56 Length: 1371  
 Score: 621.00 Matches: 151  
 Percent Similarity: 50.11% Conservative: 86  
 Best Local Similarity: 31.92% Mismatches: 210  
 Query Match: 8.78% Indels: 26  
 Gaps: 5

US-10-066-521-6 (1-1344) x US-08-795-395-1 (1-1371)

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Qy 625 AsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTrpLeuArgLysIle 644
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Qy 645 ArgValAspValLysGlyIlePheProArgAspLysSerAlaGluAlaCysProValVal 664
Db 40 CGG-----TGCAGAGCTCTCCGCTGCTC 66
Qy 665 ProLeuTrp-----MetArgAspLysThrLeuIleGlnGlnTrpGluAsp 680
Db 67 CAGCAGATAGAGGTGTCAGGCTGACGACGTCGCGCTCAGCAGAGAGCACTGCAAGAGAC 126
Qy 681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLysSerIle 700
Db 127 ATCGATTCTGCTCCGCGGCCAACCCCTCCCTGACCGAGCTGTGCTCCGACCAACGAG 186
Qy 701 LeuThrGluArgAlaMetLysThrLeuCyAlaLysLeuArgHisProThrCysLysIle 720
Db 187 CTGGGCGAATGCCGCGCGTGCACCTGTGTGCTGAGAGGCTGACAGAGCCCACTGTGAATC 246
Qy 721 GlnThrLeuMetPheArgAsnAlaGlnIleThr---ProGlyValGlnHisLeuTrpArg 739
Db 247 CAGAGAGCTCAGCCTGAGAACTGCTCCCTGACCGAGCGGGGCTCGGGGTCTGCCAGC 306
Qy 740 IleValMetAlaAsnAlaGlnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlu 759
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Db 367 GCCGCGCTGCGGCTGTGTGAGGGGCTCTGTGAGCCCAAGCTGACCTGGAAGAAGCTG 426
Qy 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysArgLeuLysLysSerGlnIleLeuThr 799
Db 427 CAGTTGAGATACGCGCGCTGAGCGCGCAGAGCTGAGGCCCTCGGCTGTGCTCAGG 486
Qy 800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
Db 487 GCCACGCGGCGCTTGAAGAGAGCTCACGATGACAAACAGCATGCGGAGCGCGGCC 546

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Qy 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
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Db 1147 AGCAGCCTCGCTGCTCTCTGTGGCCCAACCGCAGCTCGCAGACTGAGTGAAGCAAC 1206
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Qy 1080 GluGluValGlnLeuLeuIlePro-----ArgValAla 1090
Db 1327 CAGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,731
FILING DATE: (Herewith)
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,395
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/794,546
FILING DATE: 03-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,057
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942,3440003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1371 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-08-910-731-7

Alignment Scores:
Pred. No.: 4,18e-55 Length: 1371
Score: 612.00 Matches: 152
Best Local Similarity: 49.26% Conservative: 81
Query Match: 32.14% Mismatches: 214
DB: 8.65% Indels: 26
Gaps: 5

US-10-066-521-6 (1-1344) x US-08-910-731-7 (1-1371)
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Qy 645 ArgValAspValIleGlyIlePheProArgAspGlnSerAlaGluAlaCysProValAla 664
Db 40 CGG-----TGACAGAGCTCTGCGCTGCTC 66
Qy 665 ProLeuTrp-----MetArgAspIleThrLeuIleGlnGlnTrpGluAsp 680
Db 67 CAGCAGTATGAGGTGTGAGGCTGAGAGCTGCGGCTCAGAGAGAGAGAGAGAGAGAGAG 126
Qy 681 PheCysSerMetLeuGlyIleHisProHisIleuArgGlnLeuAspLeuIleSerSerIle 700
Db 127 ATCGATTCTGCCCTCCGCGCCCAACCCCTGACCGGAGCTGTGCTGTGCGACGAG 186
Qy 701 LeuThrGlnArgAlaMetIleThrLeuCysValAlaIleAsnArgHisProThrCysValIle 720
Db 187 CTGGGCGATGCGCGGCGTGCACCTGTGTGAGAGGCTGCGAGAGCCCACTGCAAGATC 246
Qy 721 GlnThrLeuMetPheArgAsnAlaGlnIleThr--ProGlyValGlnHisLeuTrpArg 739
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Qy 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeuIleGln 759
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Qy 818 GlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeu 837
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Qy 838 LeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSer 857
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Qy 858 AsnArgSerLeuThrHisLeuLysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAsn 877
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Db 976 ACAGCCGCTGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1035
Qy 978 LeuAspLeuThrAspAsnAlaLeuGlyValAspGlyValAlaAlaLeuCysGluGlyLeu 997
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RESULT 12  
 US-09-799-451-870  
 ; Sequence 870, Application US/09799451  
 ; Patent No. 6783969

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/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Zhang, Jie
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Zhao, Qiang A.
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Ma, Yundong
/ APPLICANT: Yamazaki, Victoria
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Ghosh, Reena
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6783969el Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 803
/ CURRENT APPLICATION NUMBER: US/09/799,451
/ CURRENT FILING DATE: 2001-03-05
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: pc_files Version 2.0
/ SEQ ID NO 870
/ LENGTH: 3156
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (478)..(2565)
/ US-09-799-451-870

Alignment Scores:
Pred. No.: 3,04e-32 Length: 3156
Score: 406.00 Matches: 286
Percent Similarity: 35.04% Conservative: 152
Best Local Similarity: 22.88% Mismatches: 420
Query Match: 5.74% Indels: 392
DB: 4 Gaps: 55

US-10-066-521-6 (1-1344) x US-09-799-451-870 (1-3156)

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Qy 168 TrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheAspPro 187
Db 61 CTCCTCCCTCAGT---GCCCTTCTCAGCTCTTTAAACCCGAGAGCTGTGGGCGCGGTG 117

Qy 188 ArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIle 207
Db 118 CAGACAGGTGTCTGTATGAGACAGTGGGACAGGAGAGACAGCTGTGTGCGCAAGT 177

Qy 208 ValLeuCysTrpAlaGlnGlyLysLeuTrpGlnGlyMetPheSerTrpValPhePheLeu 227
Db 178 GTTCTGAGCTGTGTATGAGGCGGCTGCG-----GCATTGAGCTGCTCATC 225

Qy 228 Pro-----ValArgLysMetGlnArgLysValGluSerSerValThrGlu 242
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Qy 243 PheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet----- 259
Db 283 CTGTGGCGCCAGCGCTAC-----ACGCTCTGAAGAGAGTTCGCTGCTCATATG 330

Qy 260 ---SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerVal 278
Db 331 GCTGCTGTGAGGTCCACACTCTCTTGTGTCTCATATGCTTATAGAGCAT----- 378

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Qy 980 LeuThrAspAlaAlaLeuGlyAspGlyGlyValAlaAlaLeuCysGluGlyLeuLysGln 999
Db 2164 GTGGCGTACACAGCTGCTGCTGAGACACAGCGCCCTGGCCCTGGCCAGAGCTGCCGGGAG 2223
Qy 1000 LysAsnSer----- 1002
Db 2224 CACCTTCCTCGAAGCTGCTACACCTTCAATGAGCTGAGCTGAGAGCGCCGCGCAG 2283
Qy 1003 ValLeuThrArgLeuGlyLeuLysAlaCysGly-----LeuThr 1015
Db 2284 GTCTTGGAGAGCTGGGGGGGCTGCTGAGAGTGGTCCCGGGTGGTGGTGTCTGACAGCA 2343
Qy 1016 SerAspCysCys-----GlnAlaLeuSerLeuAlaLeuSer-----CysAsnArgHisLeu 1032
Db 2344 GAGGGAGCGCGGTGTGAGAACTAGTCTGATCTCTGATGAAGTCCAGCGGAACTCTC 2403
Qy 1033 ThrSerLeuAsn-----LeuValGlnAsnAspHe 1042
Db 2404 AATGCTGGAGATCGGGCCGGGTTCAAGGACACCTTGAGCTCTACGCGGATCTGGA 2463
Qy 1043 SerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGln 1062
Db 2464 GATAGCCGGGT-----GCCACCTTAATCTTGGCGGCAAGGCCAG 2505
Qy 1063 IleIleGlyLeuTrpLysTrpGlnTrpValGlnIleArgLysLeuLeuGluGlnVal 1082
Db 2506 CTGCTG-----CGAGTGAAGGCGCGGCTCAAGGCGCTCTCTGAGAGCTG 2550
Qy 1083 GlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAspGlnAspAsp 1102
Db 2551 -----GMAAGCTGTGAAAGCTGAGACCTGGCGGC 2580
Qy 1103 ArgHis-----LysIleGlyLeu-ThrPheArgLeuProGluSerArgAlaTr 1118
Db 2581 AGGCACTGAGTATGACACCTGCGCTTAACCTTTCCCTC----- 2623
Qy 1118 pProCysAlaLeuLeuTrpGlyMetAsnProGluGlnLysLysArgValSerLeuLeuAl 1138
Db 2624 -----TGTGGCTCTCGCTGGCTGACGTGCTCCTTAAGAAAGATCTCTGAGGTCTGAGGC 2679
Qy 1138 ArgLysAspPhe-LysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsn 1158
Db 2680 AGAGGAATGGGCATAGCTGAGACCAAGTGCCTCTAGGGCATGTTTGACAGAGACTGAGT 2739
Qy 1158 LysGluSerGlnValAspAsnValGluGln-SerSerProGlnProMetAlaGlyThr 1177
Db 2740 CTGGAATCTCCAAAGTAAAGATGATGAATCAATGCTTGGGCTTGGAGATG----- 2790
Qy 1178 GlnHis-----LysGlnAspLysMetLeuSerValGlyTyrSer 1190
Db 2791 GAACATGCTCTCTCCATTCATTCAGCTGAGAGCAAGCAAGCATTTGGCATTTGAGGCGAG 2850
Qy 1191 GlyAlaTrp-SerGluThrAlaGluLeuGluGlyLeuGlySerAsnSerAlaAsp----- 1208
Db 2851 AGTCCCTGAAAGCACCTACCAACTTGCCTCCCTCTCTCAAAAGAGCCTTGATTTG 2910
Qy 1209 -----HisAspHisGly-----GlyMetAl 1215
Db 2911 TGTCAACCAAGGGCTCACATTTATGTTGCTGCATGCCAGGGGTGTGCCCATCCAGATTTG 2970
Qy 1215 ATPSerLeuGlyArgGluLeuSerSerArgLysLeuCysProThrValLeuMetThrTh 1235
Db 2971 TTGAAGCTT-----CCCTCTGCTTATGCTACCTGTGAGC 3009

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Qy 1235 rAlaValCysProGlyHisTrp 1242
Db 3010 ACCGAGGATGCCCTCACATTTGG 3031

RESULT 13
US-09-245-281-42
; Sequence 42, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-245-281-42

Alignment Scores:
Pred. No.: 3,63e-29 Length: 4141
Score: 379.50 Matches: 253
Percent Similarity: 37.01% Conservative: 150
Best Local Similarity: 23.23% Mismatches: 416
Query Match: 5.36% Indels: 273
DB: Gaps: 46

US-10-066-521-6 (1-1344) x US-09-245-281-42 (1-4141)
Qy 6 SerLeuThrPheSerSerTrpGlyLeuGlnTrpCysLeuTrpGluLeuAspLysGluGlu 25
Db 451 AGCTGACAGAGCTCGAAAGATCTTAAGCTGTGC----- 486
Qy 26 PheGlnThrPheLysGluLeuLysLysSerSerGluSerThrThrCysSerIle 45
Db 487 -----AAGCAAGGCGAGGAGCGTGTGAGTTCTTCTCTACGTCGCGAG- 533
Qy 46 ProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuHisGluTrp 65
Db 534 -----CAGCTGAGAGATGCTTACGTGAGC--CTCAGGCTG----- 566
Qy 66 TyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArg 85
Db 567 -----TGCTCTCAAAATTTGGCTTCTCCCTCCAGCTCATTTGG 608
Qy 86 ThrLeuSerGlyLysAlaArgAspAspMetLysLysIleSerGlnAlaMetGluGlnGlu 105
Db 609 ACCAAACTATTCGTCATATCTGACCCAGTAAAGCAAGATATCCCAAGCTGCGACACCA 668
Qy 106 GlyAlaThrAlaAlaGluThrGluGluGluGluLysSerGlnAlaMetGluGluGlu 125
Db 668 ----- 668
Qy 126 AlaThrAlaAlaGluThrGluGluGluGlyHisGlyGlyAspThrTrpAspTyrLysSer 145
Db 669 -----CTGGGCGCGGAGC-----TCC 683
Qy 146 HisValMetThrLysPheAlaGluGluGluLysAspValArgArgSerPheGluAsnThrAla 165

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Dh 684 AAGTTCATGCTGTCTACGCCCAAGAGGAGCACTG-----CTGCTGGAGAGAAC--- 734  
Qy 166 AlaAspTrpProGluMetGlnThrLeuAlaGly-----AlaPheAspSerAspArgTrp 183  
Dh 735 -----TAAATGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAGAAACCTG 782  
Qy 184 GlyPhe-----Arg 186  
Dh 783 GGCAGCCTAGAGAGCCTGAGATGCTGCTGAGACCAAGTACGGGCGTCTCAAGAGCAT 842  
Qy 187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 206  
Dh 843 GCGCAAGCTGTCTGCTGCTGTTGGAGACCGGAGAGCTGATGCTCTGCTGCAAGG 902  
Qy 207 IleValLeuCyStrAlaGlnGlyLysLeuTyrrGlnGlyMetPheSerTyrrValPhePhe 226  
Dh 903 TTGCAGAGCCTCTGGGCGCTCAGGAGGTTG---ACCTCACAAGCAATTTCTTCTCAC 959  
Qy 227 LeuProValArgGluMetGlnArgLysLysGluSer-----SerValThrGluPhe 243  
Dh 960 TTCCGCTGCGCCATGTTCACTGCTTCAAGAGAGCAGCATGCTGAGTCTCAGAGACTG 1019  
Qy 244 IleSerArgLysTrp-----ProAspSerGlnAlaProValThrGluIleMet 259  
Dh 1020 CTCTTCAAGCATTTCTGCTACCCGAGAGAGACCCCGAGAGGTTCTCTTCTGCTG 1079  
Qy 260 SerArgProGluArgLeuPheIleLeAspGlyPheAspArgLysSer----- 277  
Dh 1080 CGCTTCCCAACACAGCGCTCTTCACTTTTGAACGCTCGATGAGTGCATCTCAGACTTC 1139  
Qy 278 ValLeuAsnAspThrLysLeuCyLysAspTrpAlaGlnLysGlnProPheThr 297  
Dh 1140 GACCTGAGCCGCGTCCGATAGCTGCTGCCCTGG---GAGCGGCTCACCTCTGCTGTC 1196  
Qy 298 LeuIleArgSerIleLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal 317  
Dh 1197 CTGCTGCTAACCTCTCAAGTGGAGAGCTGCTCAAGGCTGCGGCAAAATCTCTCAGCTCT 1256  
Qy 318 Arg-----AspValGlyThrGluLysLeuLysSerGlnValValSerProArgTyr 334  
Dh 1257 GCGACAGCGCGTGGAGGTCCCCCGCAGCTCTGCGCAAAAAGTG----- 1301  
Qy 335 LeuLeuValArgGlyLysSerGlyLysGlnArgIleHisLeu----- 348  
Dh 1302 ---CTGCTCGGGGCTTCTCCCAAGT-----CACCTGCGCGCTTATGCCGCGG 1349  
Qy 349 ---LeuLeuGlnArgGlyIleGlyGlnHisGlnLysThrGlnGlyLeuArgAlaIleMet 367  
Dh 1350 ATGTTCCCGGAGCGACAGCGCAGAGAGCATCTG-----CTGCAGCAGCTGGAT 1397  
Qy 368 AsnAsnArgGluLeuLeuAspGlnCySerGlnValProAlaValGlySerLeuIleCyVal 387  
Dh 1398 GCGAACCCCAACCTCTGAGCGCTGTGGGGGTGCGCTCTCTGTGATCATCTTCCGT 1457  
Qy 388 AlaLeuGln---LeuGlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeu 406  
Dh 1458 TGTTCACGACATTCAGACAGCTCTTCAAGGGCTCTCTCAGAGTCCCGAGCTGTGCT 1517  
Qy 407 ThrGlyLeuHisAlaAlaPheVal-----PheHisGlnLeuThrPro 420  
Dh 1518 GTGACCCCTGACCGATGCTTCTCTGCTGTGCTACGTAGGTGATCTGAAGCCCGCAGCCC 1577  
Qy 421 ArgGlyValValArgArgCyLeuAsnLeuGlnGluArgValVal----- 435  
Dh 1578 AGCAAGCTGTGTGACCGCAACAGCGGACCGCGGCAAAACCTTACGTGACGGCTGGCGC 1637  
Qy 436 ---LeuLysArgPheCyArgMetAlaValGlnGlyValTrpAsnArgLysSerValPhe 454  
Dh 1638 ACGGTGATGCGGTGGAGAGAGTGTCTCAGGAGCAGCAGAGAGCTCTTGTGTGTT 1697  
Qy 455 AspGlyAspArgLeuMetValGlnGlyLeuGlyLysSerGluLeuArgAlaLeuPheHis 474  
Dh 1698 GGCAGAGGAGGTGACAGCGCTCGAAGCTGCAAGAGAGATCTGCACTGGGCTTCTCTG 1757

Qy 475 MetAsnIleLeuLeuProAspSerHisCySerGlu-----GluTyrrTyrrThrPhePheHis 492  
Dh 1758 CGG-----GCTTGGCCGATGTTGGCGCTGAGAGCGGCGAGTCTTCAATTTTCTCAC 1811  
Qy 493 LeuSerIleuGlnAspPheCyAlaAlaLeuTyrrTyrrValLeuGlnGlyLeuGlnIleGlu 512  
Dh 1812 CTTAAGCTCCAGAGCTTCTTCAACCGCTTCTCTCTGTACCAAGTGAACAGTGAAGCACC 1871  
Qy 513 ProAlaLeuCyProLeuTyrrValGlnLysThrLysArgSerMetGluLeuValAla 532  
Dh 1872 CCGAGATGTCGAGAGTCTTTCAGAAATGAGACGCTCTCTGA---GAGGCAACAAGCTCG 1928  
Qy 533 GlyPheHisIle----- 536  
Dh 1929 TCTGCAATCTTCTCTTCTCTCTCAAGTCCCTGGCGGAGAAACCGGTTGGCGCT 1988  
Qy 537 -----HisSerLeuTrpMetLysArgPheLeuPheGlyLeuVal 549  
Dh 1989 GATCTTTTCAGGAACAAGATCACTTCCAGTTCAACCACTTTCGTGCGGGCTACTG 2048  
Qy 550 SerGluAspValArgArgProLeuGlnValLeuLeuGlyCyProValProLeuGlyVal 569  
Dh 2049 GCCAAAGCCGACAGAAATCTCTTCCGCACTG-----GTGCCAAGGCTATC 2096  
Qy 570 -----LysGlnLysLeuLeuHisTrpVal-----SerLeu 579  
Dh 2097 CTGAGAGAAAGCGCAAGCGCTG---TGGGCTCACCTGTTGTGCTAGCTGCCCTCTAC 2153  
Qy 580 LeuGlyGlnGlnProAsnAlaThrThrProGly-----Asp 591  
Dh 2154 TTGAAGAGCTTACCTCGGCTCACTGAGGCTTGAAGCTTAAACAGGTGCATGCCATCCACA 2213  
Qy 592 ThrLeuAspAlaPheHisCyLysPheGluThrGlnAspLysGluPheValArgLeuAla 611  
Dh 2214 TTCTGTGATGATCGCGCTGATCATTTATGAACGACAGACCAAGAGTGGCGGCTGCC 2273  
Qy 612 LeuAsnSerPheGlnGlnValTrpLeuProIle-----AsnGlnAsnLeuAsp 627  
Dh 2274 GCGAGGGGACATAGTGGAGTACCTCAAGCTGGCCTTTTGCAACGCTTGCTGCGGAC 2333  
Qy 628 LeuIleAlaSerSerPheCyLysGlnHisCyProTyrrLeuArgLysIleArgValAsp 647  
Dh 2334 TGCAGCGCGCTGTCTTCTGCTGCATCAC-----TTCAACAGGCACTGGCGCTGAC 2387  
Qy 648 ValLysGlyIlePheProArgAspGluSerAlaGluAlaCyProValProLeuTrp 667  
Dh 2388 CTGACACAACAACCTCAATGACTATGCGGTGAC-----GAGCTGCAGCTTGCTTT 2441  
Qy 668 MetArgAspLysThrLeuIleGlnGlnGlnTrpGluAspPheCySerMetLeuGlyThr 687  
Dh 2442 AGCGGT----- 2447  
Qy 688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLys 707  
Dh 2448 -----CTCAGGTTATCAGACTCAGCGTCAACCAAGATCCCGCAGGGGTTAAG 2498  
Qy 708 ThrLeuCyAlaLysLysLeuArgHisProThrCyLysValIleGlnThrLeuMet---PheArg 726  
Dh 2499 GTGCTATGTAGGAACG---ACCAAGTAAAGTCTGACGTCTCGGGTTTATAC 2552  
Qy 727 AsnAlaGlnIleThrPro---GlyValGlnHisLeuTrpArgIleValMetAlaAsnArg 745  
Dh 2553 AACCAACAGATTAAGTATATCGAGCGAGATATGTGCCAAATCTCGATGATGACGA 2612  
Qy 746 AsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGluAspValArgMetAla 765  
Dh 2613 GCGCTCAAGCACTTAATAGGGAATAACAGATAACAAGTAGCGGGAAGTGTGTG 2672  
Qy 766 CySerGlnAlaLeuLysHisProLysCyLysLeuLeuGluSerLeuArgLeuAspCyGly 785  
Dh 2673 GCTTGGCTGTGAAGAC----- 2690

Qy	786	LeuthrHnSaLaCyTyLeuLylLeuSerGlnLeuThrThSProSerLeu	805
Db	2691	-----AGCACTCCATCGTT	2705
Qy	806	SeLSeuSerLeuAlaGlyAsnLylValThrApGInGlyValMetProLeuSerAspAla	825
Db	2706	GATGTGGGATGTGGGTTATCATGATTGGAGACAGAGGGCAAGGCGCTTGACAGAGCA	2765
Qy	826	LeuHrGValSerGInCyAlaLeuGInLylLeuLylLeuGluAbpCyGlyTLeThrAla	845
Db	2766	TTGAAG--GACCAACCCAGCGCTTGACACTCTCACTGATTCGATTCAAAGGATCTTCGG	2822
Qy	846	ThrGInCySgInSerLylAserLAlaLeuValSerAsnApSerLeuThrHlLeuLys	865
Db	2823	GAGGAGGGAAGAGCTTGTCCGAGGCGCTTGAAACAGAACACCACTGACATGATTCGG	2882
Qy	866	LeuSerAsnAsnSerLeuGlyValAsnGluGlyValAsnLeuLeuCyAbpSerMetArgLeu	885
Db	2883	CTGACCAAAATGAACTTAATGATATGCTGTGACAGTGTCTTCGTAAGATGTGAGACTG	2942
Qy	886	ProHlScySerSerLeuGInArgLeuMetLeuAsnGInCyAbpLeuAbpThrAlaGlyCys	905
Db	2943	--AACCAAGCGCTACGCGCATTTATGCTGATCCAGATTCACATCAGACCAAGGAGACA	2999
Qy	906	GlyPheLeuAlaLeuAlaLeuMetClyAsnSerTrpLeuThrHlLeuSerLeuSerMet	925
Db	3000	GCGCAGCTGGGGAGGGCATCTGACAGAAACACAGCCATTAACAGAGATTGTCTCAATGGA	3055
Qy	926	AsnProValGlu-----AspAsnGlyValLylLeuLeuCySgIn	938
Db	3060	AACTTGATTTAAGCCCGAGAGAGGCCAAATCTTCAGAAATGAGAAAGAAATATCTGCTT	3118
Qy	939	ValMetArgLupProSerCyAbpLeuGInAbpLeu-----GluLeuValLylCyAbp	956
Db	3119	CTGACGAGAGCGCTCCGGG-----CAGATCTTGTCTCTAGGTGCTCTCAGTCAAC	3169
Qy	957	LeuThrAlaAlaCyS-----CyGluSerLeuSerCyVal	968
Db	3170	AG-ACAGACCTGTGCTGATCAGCAGGGGTAGCAGAGATCTGTGACGCGCTGCAGCAAGGTG	3228
Qy	969	ILeserArgSerArgHlLeuLylSer	977
Db	3229	CCTGTCAAGAGCCACACCTTCACAGT	3255
RESULT 14			
US-09-207-359B-42			
: Sequence 42. Application US/09207359B			
: Patent No. 6469140			
: GENERAL INFORMATION:			
: APPLICANT: Berlin, John			
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
: FILE REFERENCE: 07334-112001			
: CURRENT APPLICATION NUMBER: US/09/207.359B			
: CURRENT FILING DATE: 1998-12-08			
: PRIOR APPLICATION NUMBER: US 09/099,041			
: PRIOR FILING DATE: 1998-06-17			
: PRIOR APPLICATION NUMBER: US 09/019,942			
: PRIOR FILING DATE: 1998-02-06			
: NUMBER OF SEQ ID NOS: 47			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 42			
: LENGTH: 4141			
: TYPE: DNA			
: ORGANISM: Mus musculus			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (261)...(3119)			
US-09-207-359B-42			
Alignment Scores:			
Pred. No.:		3.63e-29	Length: 4141
Score:		379.50	Matches: 253

Percent Similarity:		37.01%	Conservative:	150
Best Local Similarity:		23.23%	Mismatches:	416
Query Match:		5.36%	Indels:	273
DB:		3	Gaps:	46

US-10-066-521-6 (1-1344) x US-09-207-359B-42 (1-4141)

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QY	26	PheGlnThrPheLysGluLeuLeuLysLysSerSerGluSerThrThyCysSerIle	45
DB	487	-----AGAGCAAAAGCCAGAGAGCTCTGAGTCTTCTCTCACTGCTCCAG-----	533
QY	46	ProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuLeuHISgluTyr	65
DB	534	-----CAGCTGAGAGATGCTTACGCGAC-----CTCAGGCTG-----	566
QY	66	TyrGlyAlaSerLeuAlaTPrAlaThrSerIleSerIlePheGluAsnMetLeuAlaArg	85
DB	567	-----TGCGCTCCAGAAATTTGGCTTCTCCCTCCCAAGCTCATTTCCG	608
QY	86	ThrLeuSerGluLysAlaArgAspMetLysLysIleSerGlnAlaMetGluGlnGlu	105
DB	609	ACCAAAACTATGCTCAATATCTAGCCAGTACAGAGGTATACCAACAGCTGCACACCA	668
QY	106	GlyAlaThrAlaAlaGluThrGluGluGlnGlnIleSerGlnAlaMetGluGlnGlu	125
DB	668	-----	668
QY	126	AlaThrAlaAlaGluThrGluGluGlnGlnIleHISgluLysThrTPrAspTyrLysSer	145
DB	669	-----CTGGGCGCCGAC-----TCC	683
QY	146	HISValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGluAsnThrAla	165
DB	684	AAATTCAATGCTGTGCTACGCCCAAGAGAGACCTG-----CTGCTGAAGAGAC--	734
QY	166	AlaAspTPrProGluMetGlnThrLeuAlaGly-----AlaPheAspSerAspArgTPr	183
DB	735	-----TATATGGACACATCATAGGGGCTGTAGGCTTCAACATGAAAACTG	782
QY	184	GlyPhe-----	186
DB	783	GGCAACCTAGAGAGCCTGGATTCCTGTGACACACATGACGGCGCTCTCAACGACAT	842
QY	187	ProArgThrValValLeuHISgluLysSerGlyIleGlyLysSerAlaLeuAlaArg	206
DB	843	GGCGAGACTGCTTGTGTGGGAGACGGGAGTGGGCAATTCATGTGCTGCAGAGG	902
QY	207	IleValLeuCysTPrAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePhe	226
DB	903	TTGCAGAGACCTCTGGGCGCTCAGGACGTTG---ACCTCAGACCCAAATTTCTTCTTCAC	959
QY	227	LeuProValArgGluMetGlnArgLysLysGluSer-----SerValThrGluPhe	243
DB	960	TTCCGCTGCCGATGTTGAGCTTCAAGAGAGAGCATGCTGATGCTGCAGAGACTG	101
QY	244	IleSerArgGluTPr-----ProAspSerGlnAlaProValThrGluIleMet	259
DB	1020	CTCTTCAAGCATTTCTGTGTAACCCGAGACGAGACCCCGAGAGAGTGTCTTCCTTCTGCTG	1077
QY	260	SerArgPTrProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuLysSer	277
DB	1080	CGCTTCTCCACACAGCGCTCTTCACTTTTGAACGGCTGGATGAGCTGCATCACTCACTTC	113
QY	278	ValLeuAsnAspThrLysLeuCysLysAspTPrAlaGluLysGluInProPhePheThr	297
DB	1140	GACCTGAGCCCGGATCGGATATGCTGTGCCCTGG---GAGCCGGCTCAACCTCGTGC	119
QY	298	LeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrVal	317



QY 957 LeuThrAlaAlaCys-----CysGluSerLeuSerCysVal 968  
 Db 3170 AG-ACAGCATGTGTGACGTACAGAGGTAGCATGTGTGAGCGCTGTGACGACGAGGTG 3228  
 QY 969 ILeSerArgSerArgHisLeuLeuSer 977  
 Db 3229 CCTGTCAAGAGCCACACCTCCACAGT 3255  
 RESULT 15  
 US-09-340-620A-42  
 ; Sequence 42, Application US/09340620A  
 ; Patent No. 6482933  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Berlin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-124001  
 ; CURRENT FILING DATE: 1999-06-28  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/245,281  
 ; PRIOR FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/207,359  
 ; PRIOR FILING DATE: 1998-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/099,041  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: US 09/019,942  
 ; PRIOR FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: PasteSeq for Windows Version 4.0  
 ; SEQ ID NO 42  
 ; LENGTH: 4141  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURES:  
 ; NAME/KEY: CDS  
 ; LOCATION: (261)...(3119)  
 ; US-09-340-620A-42  
 Alignment Scores:  
 Pred. No.: 3,636-29 Length: 4141  
 Score: 379.50 Matches: 253  
 Percent Similarity: 37.01% Conservative: 150  
 Best Local Similarity: 23.23% Mismatches: 416  
 Query Match: 5.36% Indels: 273  
 Gaps: 46  
 US-10-066-521-6 (1-1344) x US-09-340-620A-42 (1-4141)  
 QY 6 SerLeuThrPheSerSerTyrglyLeuGlnTrpCysLeuTyrglyLeuAspIleGlu 25  
 Db 451 AGCTGACAGAGTCCGAAGAATCTTGACCTGTGC----- 486  
 QY 26 PheGlnThrPheIleGlyLeuLeuIleuIleuSerSerGluSerThrCysSerIle 45  
 Db 487 -----AGAGCAAAAGCGAGAGGTGTCTGATCTTCTCTTACGTGCTGAG- 533  
 QY 46 ProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeuLeuHisGluTyr 65  
 Db 534 -----CAGCTGAGAGATGCTTACGTGAC--CTCAGAGCTG----- 566  
 QY 66 TyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArg 85  
 Db 567 -----TGCTCTCAGAAATTTGGCTTCTCCCTTCCACGCTACTTGG 608  
 QY 86 ThrLeuSerGlyValAlaArgAspArgMetLeuIleValIleSerGlnAlaMetGluGln 105  
 Db 609 ACCAAACTATCTGCTCAATATGACCCAGTACAGAGTATACCAACAGCTGCACACCA 668  
 QY 106 GlyAlaThrAlaAlaGluThrGluGluGlnGluIleSerGlnAlaMetGluGlnGly 125  
 Db 668 ----- 668  
 QY 126 AlaThrAlaAlaGluThrGluGluGlnGluIleGlyGlyAspThrTrpAspTyrLeuSer 145  
 Db 126 ----- 145

Db 669 -----CTGGCCCGCGAC-----TCC 683  
 QY 146 HisValMetThrIlePheAlaGluGluIleValAlaArgSerPheGluAsnThrAla 165  
 Db 684 AAGTTCACTGTGTGTACGCCAAGAGAGACTG-----CTCCTGAGGAGACC--- 734  
 QY 166 AlaSerTrpProGluMetGlnThrLeuAlaGly-----AlaPheAspSerAspArgTrp 183  
 Db 735 -----TATATGACACACTATGGGGGCTGTAGGCTTCAACAATGAAAACCTG 782  
 QY 184 GlyPhe-----Arg 186  
 Db 783 GGCAGCCTTAGAGAGCCTGATGCTCTGTGACCAAGTACGAGCGGCTCTCAACAGCAT 842  
 QY 187 ProArgThrValValLeuHisGlyIleuSerGlyIleGlyIleuSerAlaAlaArgArg 206  
 Db 843 GCGGAGACTGTCTTCTGTGGGAGCCGGAGGGAGGAGTTCATGCTGTGACAGG 902  
 QY 207 IleValLeuCysTrpAlaGlnGlyIleuTyrglnGlyMetPheSerTrpValPhePhe 226  
 Db 903 TTGCAGAGCCTCTGGGCTCAGGAGGTG--ACCTCAGACGCCAATTTCTTCCAC 959  
 QY 227 LeuProValArgGluMetGlnArgIleuIleuSer-----SerValThrGluPhe 243  
 Db 960 TTCCGCTCCCGCATTTCACTGCTTCAAGAGAGCAGATGCTGAGCTCAGGAGCCTG 1019  
 QY 244 ILeSerArgGluTrp-----ProPheSerGlnAlaProValThrGluIleMet 259  
 Db 1020 CTCTTCAAGCATTTCTGTCTACCCGAGAGAGACCCGAGAGGTCTTCTCTTCTGCTG 1079  
 QY 260 SerArgProGluArgLeuLeuPheIleLeuAspGlyPheAspAspLeuGlySer----- 277  
 Db 1080 CGCTTCCCAACACAGCGCTTTCACCTTTACCGCTCGATGAGTCACTCACTCAGACTTC 1139  
 QY 278 ValLeuAsnAsnAspThrIleLeuCysIleAspTrpAlaGluIleGlnProPheThr 297  
 Db 1140 GACCTGAGCCCGCGCCGATAGCTGCTGCCCTGG--GAGCGCGCTCACCTCTGTGTC 1196  
 QY 298 LeuIleArgSerLeuLeuArgIleValLeuLeuProGluSerPheLeuIleValThrAla 317  
 Db 1197 CTGCTGCTAACTCTCTAAGTGGAGAGCTGTCAAGGTTGCCGGAATTTGCTCACTCT 1256  
 QY 318 Arg-----AspValGlyThrGluIleuIleuSerSerGluValIleSerProArgTyr 334  
 Db 1257 CGCACAGCGCTGAGAGTCCCCCGCCAGCTCTCGCCAAAGGTG----- 1301  
 QY 335 LeuLeuValArgGlyIleSerGlyLeuGlnArgIleHisLeu----- 348  
 Db 1302 ---CTGCTCGGGGCTTCTCCCAAGT-----CACTGCGCGCCTATGCCGCCGG 1349  
 QY 349 ---LeuLeuGluArgGlyIleGlyGluHisGlnIleuIleuIleuIleuIleuIleuIleu 367  
 Db 1350 ATGTTCCTCCCGCCGACAGCCGACAGAGCATGTG-----CTGCACAGCTGAT 1397  
 QY 368 AsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal 387  
 Db 1398 GCCAACCACCAACTGTGAGCCTGTGGGGTGGCGCTCTTGTGATATCTTCCGT 1457  
 QY 388 AlaLeuGln---LeuGlnAspValValGlyIleuSerValAlaProPheAsnGlnThrLeu 406  
 Db 1458 TGTTCAGACACTTCAGAGAGTCTTGAAGGCTCTTCAAGTTGCCGAGCTGCT 1517  
 QY 407 ThrGlyLeuHisAlaAlaPheVal-----PheHisGlnLeuThrPro 420  
 Db 1518 GTGACCTGACCGATGCTTCTGTCTGTGTCACTGAGTGCATGACAGCCCGACGCC 1577  
 QY 421 ArgGlyValValArgArgCysLeuAsnLeuGluIleuArgValVal----- 435  
 Db 1578 AGCAGCCTGTGTGCGGACAGCAGCGCAGCCGCGGAAACCTTACGTCAGCGCTGGCGC 1637  
 QY 436 ---LeuIleArgPheCysArgMetAlaValGluIleValTrpAsnArgIleValPhe 454  
 Db 1638 ACGCTGATGCGCTGGGAGAGTGTCTCACAGGAGCAGCAAGAGCTCTTGTGTGTT 1697

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Qy 455 AspglyAspArgLeuMetValGlnGlyLeuGlyGlnSerGluLeuValAlaLeuPheHis 474
Db 1698 GCGCAGGAGGAGGTGCGAGGCGCTCGAAGCTCGAAGAGATCTGCACTGGGCTTCCTG 1757
Qy 475 MetAsnIleLeuLeuProAspSerHisCysGlu-----GluTyrTyrThrPhePheHis 492
Db 1758 CGG-----GCTTGGCCCGATGTGGGCCCTTAGCAGGCGCCAGTCTTACGAATTTTTCAC 1811
Qy 493 LeuSerLeuGlnAspPheCysAlaIleuTyrTyrValLeuGlnGlyLeuGluIleGlu 512
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Qy 513 ProAlaLeuCysProLeuTyrValGlnGlyLeuThrLeuValSerMetGluLeuGlnAla 532
Db 1872 CGGAGGTGTGAGAGTTCTTTCGAAATGACGTCTCTGGA---GAGGCAACAAGCTCG 1928
Qy 533 GlyPheHisIle----- 536
Db 1929 TCCTGCCATTCTTCTCTTCTCTTCCAGTCCGCGGCGGAGAAAGCGGTTGGCCCT 1988
Qy 537 -----HisSerLeuTrpMetLeuValArgPheLeuPheGlyLeuVal 549
Db 1989 GATCCTTTCAGGAACAAGATCACTTCCAGTTTCACCAACCTTCTGTCGCGGCTACTG 2048
Qy 550 SerGluAspValAlaArgArgProLeuGlnValLeuLeuGlyCysProValProLeuGlyVal 569
Db 2049 GCCAAAGCCCGACAGAAACTCTTCGCGAGCTG-----GTCCCAAGGCTATTC 2096
Qy 570 -----LysGlnLeuLeuHisTrpVal-----SerLeu 579
Db 2097 CTGAGAGAGAAAGCGCAAGGCCCTG---TGGGCTCACTGTTTCTAGCCTGCGCTCTTAC 2153
Qy 580 LeuGlnGlnGlnProAsnAlaThrThrProGly-----Asp 591
Db 2154 TTGAAGAGCCCACTCGGCTCCAGTCCAGTCCAGGCTTTAACAGAGTCATGCCATGCCACA 2213
Qy 592 ThrLeuAspAlaPheHisCysLeuPheGlnThrGlnAspLysGlnPheValAlaArgLeuAla 611
Db 2214 TTCCCTGGAGATCGCGCTGCATCATATGACAGCAGACAGAAAGTGGCGGCTCGCC 2273
Qy 612 LeuAsnSerPheGlnGlnValTyrLeuProIle-----AsnGlnAsnLeuAsp 627
Db 2274 GCCAGGCGCATCACTGCGGATCACTCAAGCTGGCTTTTGCAACGCTTGTCTGCGGAC 2333
Qy 628 LeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuAlaArgLysIleAlaValAsp 647
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Qy 648 ValLysGlyIlePheProArgAspGlnSerAlaGluAlaCysProValValProLeuTyr 667
Db 2388 CTGACACAACAACAACCTCAATGATATGCGTGCAG-----GAGCTGCACGCTTGTCTT 2441
Qy 668 MetArgAspLysThrLeuIleGlnGlnIleTyrGlnAspPheCysSerMetLeuGlyThr 687
Db 2442 AGCCGT----- 2447
Qy 688 HisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnAlaArgAlaMetLys 707
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Qy 708 ThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMet---PheArg 726
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Qy 727 AsnAlaGlnIleThrPro---GlyValGlnHisLeuTyrArgIleValMetAlaAsnArg 745
Db 2553 AACCAACGATTAATGATATGATGAGCCAGTATGCGCCAAATCTTGATGAATGCGAGA 2612
Qy 746 AsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGluAspValAlaArgMetAla 765
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Qy 786 LeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLys 805
Db 2691 -----AGACCTCCATGCTT 2705
Qy 806 SerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAla 825
Db 2706 GATGTTGGAGATGTGGGGTAAATCAGATTGAGACGAAGGCGGCAAGGCTTGCGAGAGCA 2765
Qy 826 LeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyIleThrAla 845
Db 2766 TTGAAG---GACCAAGCCAGCTGACCACTTCAGTCTTGCAATTCAATGGCATCTCCG 2822
Qy 846 ThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCys 865
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Qy 866 LeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeu 885
Db 2883 CTGACCAAAATGAATTAATGATGATGTGCAAGAGTCTTCGCTGAGATGCTAGAGTGTG 2942
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Qy 906 GlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMet 925
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Qy 926 AsnProValGlu-----AspAsnGlyValLysLeuLeuCysGlu 938
Db 3060 AACTTGAATTAAGCCCGAGAGGCAAGAGTCTTGCAAGATGAGAGAGATCATCTGCTT- 3118
Qy 939 ValMetArgLysProSerCysHisLeuGlnAspLeu-----GluLeuValLysCysHis 956
Db 3119 CTGACGGAAGCTCTCTGGG-----CAGGATCTTGTCTCTAGTGTCTCTCAGTCAAC 3169
Qy 957 LeuThrAlaAlaCys-----CysGlnSerLeuSerCysVal 968
Db 3170 AG-ACAGCACTGTCACTACAGAGGTAAGCAAGATGCTGTGACAGCGCTGCAGCAAGGTG 3228
Qy 969 IleSerArgSerArgHisLeuLysSer 977
Db 3229 CCTGTCAAGAGCCCAACCTCCACAGT 3255

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Search completed: February 4, 2005, 18:11:52  
 Job time : 670 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p1ue\_p2n model

Run on: February 4, 2005, 17:27:06 | Search time 1551 Seconds

(without alignments)  
4987.568 Million cell updates/sec

Title: US-10-066-521-6

Perfect score: 1 MEGDRLS/TFSSYGLQWCLYR.....DDHSGVMSLGAAGLEGLVS 1344

Sequence:

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPRO.spool/h/US10066521/runac\_04022005\_114554\_4440/app\_query.fasta\_1.1543  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=std.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloum62  
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HARPSIZE=500 -MINLEN=0  
-MALIGN=200000000 -USER=US10066521@cgn2\_1.1.876@runac\_04022005\_114554\_4440  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published Applications NA.\*

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22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7074	100.0	4035	14	US-10-124-498-5
2	7074	100.0	4035	14	US-10-066-521-5
3	5756	81.4	3489	17	US-10-416-642-3
4	5756	81.4	3926	15	US-10-216-645-1
5	5741.5	81.2	3885	18	US-10-660-761-3
6	5741.5	81.2	3900	17	US-10-399-443-23
7	5741.5	81.2	3900	17	US-10-677-943-23
8	5683.5	80.3	3830	15	US-10-216-645-3
9	5120	72.4	3226	17	US-10-092-900A-347
10	2688	38.0	3447	17	US-10-399-443-5
11	2688	38.0	3447	17	US-10-677-943-5
12	2005	28.3	1157	17	US-10-399-443-1
13	2005	28.3	1157	17	US-10-677-943-1
14	1885.5	26.7	3521	18	US-10-794-342-2
15	1435	20.3	3368	14	US-10-124-498-23
16	1435	20.3	3368	14	US-10-066-521-23
17	1434	20.3	2982	14	US-10-124-498-25
18	1434	20.3	2982	14	US-10-066-521-25
19	1434	20.3	2985	10	US-09-965-621-15
20	1434	20.3	2985	17	US-10-407-866-15
21	1402	19.8	2775	17	US-10-781-294-15
22	1402	19.8	2775	17	US-10-357-820-51
23	1335	18.9	1075	17	US-10-399-443-3
24	1335	18.9	1075	17	US-10-677-943-3
25	1332.5	18.8	3484	18	US-10-794-342-3
26	1320.5	18.7	3108	10	US-09-965-621-23
27	1320.5	18.7	3108	17	US-10-407-866-23
28	1320.5	18.7	3108	18	US-10-781-294-23
29	1316.5	18.6	3190	17	US-10-094-749-1079
30	1315.5	18.6	3172	18	US-10-398-037-74
31	1314.5	18.6	2883	17	US-10-161-993-3
32	1313.5	18.6	3540	18	US-10-794-342-7
33	1304.5	18.4	3218	17	US-10-407-866-67
34	1303.5	18.4	3186	14	US-10-124-498-17
35	1303.5	18.4	3186	14	US-10-066-521-17
36	1289.5	18.2	2575	9	US-09-848-035-7
37	1289.5	18.2	2575	9	US-09-966-224-7
38	1255	17.7	3102	13	US-10-127-516-6
39	1255	17.7	3102	13	US-10-027-629-6
40	1255	17.7	3102	16	US-10-132-967-6
41	1255	17.7	3857	13	US-10-127-516-4
42	1255	17.7	3857	13	US-10-027-629-4
43	1255	17.6	3189	15	US-10-132-967-4
44	1248.5	17.6	3189	15	US-10-239-663-10
45	1242	17.6	3466	17	US-10-108-260A-718

#### ALIGNMENTS

RESULT 1  
US-10-124-498-5  
; Sequence 5, Application US/10124498  
; Publication No. US20030017983A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Weiye  
; APPLICANT: Berlin, John  
; APPLICANT: Blacher, Maria  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
; FILE REFERENCE: 07334-367001  
; CURRENT APPLICATION NUMBER: US/10/124,498  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 10/066,521  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/318,645  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/265,231  
; PRIOR FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 25

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; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
US-10-124-498-5

Alignment Scores:
Pred. No.: 0 Length: 4035
Score: 7074.00 Matches: 1344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

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QY 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysSerSerGluSer 40
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QY 41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
Db 121 ACCCAAGCTTATTTCACAGATTGAAATCGAAATGCGAAGTGGAAATGCTTGGCACTC 180

QY 61 LeuLeuHisGluTyrglyTyrglyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
Db 181 CTCCTGATGATGATTTATGAGATCGCTGGCTGGGCTACGTCATTAGCATCTTTGAA 240

QY 81 AsnMetAsnLeuAlaGlnThrLeuSerGluLysAlaArgAspAspMetLysLysIleSerGln 100
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QY 101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnIleSerGluAla 120
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QY 121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGlnGlyHisGlyGlyAspThr 140
Db 361 ATGAAACAAGAAAGGCGCACAGCACAGACAGAAACAGAAACATGGAGTACACA 420

QY 141 TrpAspTyrllysSerHisAlaMetThrLysPheAlaGluGluAspValArgArgSer 160
Db 421 TGGGACTTACAAAGATTCAGTATGACCAATTCCCTGAGAGAGATGTAAGTCTGTAGT 480

QY 161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
Db 481 TTGAAACACTGCTGCTGCTGCTGCGGAAATGCAACGTTGGCTGGTCTTTGATTCA 540

QY 181 AspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLys 200
Db 541 GACGGGAGGGGCTTCCGGCTCGCACGGTGGTTTGACACGGAAGTCAAGAAATTGGGAAA 600

QY 201 SerAlaLeuAlaArgAlaGluLeuValLeuCysTrpAlaGlnGlyLysLeuTyrglnGlyMet 220
Db 601 TCGGCTCTAGCCAAAGAGATGCTGTGCTGGCGCGCAAGGTGAGCTCTTACCAAGGAATG 660

QY 221 PheSerTyrlValPhePheLeuProValArgGluMetGlnArgLysLysGluSerSerVal 240
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QY 241 ThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMetSer 260
Db 721 ACAGAGTTCACTCTCAGAGAGTGGCCACATCCCAAGCTCCGGTGCACGAGATCATGTCC 780

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Db 841 AATGACACAAAGCTCTCCAAAGACTGGGCTGAGAAAGACGCTCCGTTCACTCATAGCC 900

QY 301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValArgAspVal 320
Db 901 AGTCTGCTGAGAAAGTCTGCTCTCCGATGAGTCTTCTGTATGTCACCGGACAGAGAGTGG 960

QY 321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrlLeuLeuValArgGlyIle 340
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QY 521 GluLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp 540
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QY 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db 1621 ATGAAGCGTTTCTTGTGGCTCTGTGAGCGAAAGACGTAAAGAGGCACTGAGAGTCTTG 1680

QY 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580
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QY 601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620
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QY 621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrl 640
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Qy ValMetAlaAsnArgAsnLeuArgSerIleuAsnLeuGlyIleThrHisIleuLeuGluGln 760  
Db 2221 GTCATGGCCAAACCGTAACCTTAAGATCCCTCAACTGGGAGGACCCACCTGAAAGAGAG 2280  
Qy AspValArgMetAlaCysGluAlaIleuIleHisIleProIleCysIleuLeuGlnSerIleuArg 780  
Db 2281 GATTTAAGAGATGGGGGTGAAGCTTAAACACCCAAATGTTGTGGAGATCTTTTGAAG 2340  
Qy LeuAspCysCysGlyIleuThrHisAlaCysIleuIleSerGlnIleSerGlnIleuThrThr 800  
Db 2341 CTGGATTTGCTGTGATGATACCCATGCTGTTTACCTGAAAGATCTCCCAATCTTTACAGAC 2400  
Qy SerProSerIleuIleSerIleuSerIleuAlaGlyIleuIleValIleThrAspGlnIleValMet 820  
Db 2401 TCCCCAGCGCTGAATCTCTGAGCTGGCAGAGAAACAAAGTGACAGACAGGAGTAAATG 2460  
Qy ProLeuSerAspAlaIleuArgValIleSerGlnCysAlaIleuGlnIleuIleuIleuGluAsp 840  
Db 2461 CCTTCAGTAAATGCTTGAAGGTCTCCAGTGGCCCTGACAAAGCTGATCTGGAGAGAC 2520  
Qy CysGlyIleThrAlaThrGlyIleGlnIleSerIleuAlaSerAlaIleValIleSerAsnArgSer 860  
Db 2521 TGTGGCATCACAGCCAGGGTGGCCAGAGTCTGGCTCAGGCCCTGCTGACAGACCGGAGC 2580  
Qy LeuThrHisIleuCysIleuSerAsnAsnSerIleuGlyIleAsnGluGlyValIleAsnLeuCys 880  
Db 2581 TTGACACACCTGTGCTATTCACACAGCTGGGGAAACAAAGGTGTAATCTACTGTGT 2640  
Qy ArgSerMetArgIleuProHisIleuSerIleuGlnArgIleuMetIleuAsnGlnCysHisIleu 900  
Db 2641 CGATCCATGAGGCTTCCCACTGATGCTGACAGAGGCTGATGCTGAATCACTGACCACTG 2700  
Qy AsnThrAlaGlyIleuGlyPheIleuAlaIleuAlaIleuMetGlyIleuAsnSerTrpIleuThrHis 920  
Db 2701 GACACGGCTGGCTGTGTCTTCTGCACTTCCGCTTAAGGTTAACTCATGTGCTGACGAC 2760  
Qy LeuSerIleuSerMetAsnProValGluAspAsnGlyValIleValIleuLeuCysGluIleValMet 940  
Db 2761 CTGAGCTTTAGCAAGAACCTGTGGAGAGCAATGGCCGTGAAGCTTTCTGTGGAGGTACG 2820  
Qy ArgGluProSerCysHisIleuGlnAspLeuGluIleuValIleCysHisIleuThrAlaAla 960  
Db 2821 AGAAGAACCATCTTGTCACTCTCAGAGACCTGAGTTGTGAAGTGCATCTCAGCCGCCG 2880  
Qy CysCysGlnSerIleuSerCysValIleSerArgSerArgHisIleuIleuValSerIleuAspLeu 980  
Db 2881 TGTCTGTAGAGTCTGTCTGTGTGATCTCGAGAGACACACTGAAAGAGCTGTGATTC 2940  
Qy ThrAsnAlaIleuGlyAspGlyGlyValAlaIleuCysGlyGluGlyIleuIleGlnIle 1000  
Db 2941 ACGGACATGCTCGGGTGAACGGTGGGTTCTGTGCTGAGAGGACTGAAGCAAAAG 3000

Qy AsnSerValIleuThrArgLeuGlyIleuIleValIleCysGlyIleuThrSerAspCysCysGlu 1001  
Db 3001 AACAGTGTTCAGAGAGACTGGGTTGAAGGCAATGGACATGCTTCAATTCGCTGTAG 3060  
Qy AlaIleuSerIleuAlaIleuSerCysAsnArgHisIleuThrSerIleuAsnLeuValGlnAsn 1040  
Db 3061 GCACCTTCCTTGGCCCTTCTTCGCAACCGGAGATCTGACCACTTAACCTGTGGAGAT 3120  
Qy AsnPheSerProIleuGlyMetIleuValIleuCysSerAlaPheAlaCysProThrSerAsn 1060  
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Db 3181 TTACAGATTAATTTGGGCTGTGAAATGGCAGTAACTCTGTGCAATTAAGAACTGCTGAG 3240  
Qy GluValGlnIleuLeuIleuProArgValValIleAspGlySerTrpHisSerPheAspGlu 1100  
Db 3241 GAGTGGAGCTACTCAAGCCCGAGTGTGTAATTAAGAGTGGATTTCTTTGATGAA 3300  
Qy AsnAspArgHisIleuGlyIleGlyIleuThrPheArgIleuProGlnIleuSerArgAlaIleProCys 1120  
Db 3301 GATGACGACCAAAATAGACCTTACTTCCGCTCCCTGAAAGCCGGGCAATGGCCATGT 3360  
Qy AlaIleuLeuTrpGlyMetAsnProGlnIleuIleValIleAspIleuAlaGlyIleAsp 1140  
Db 3361 GCTTTCGTGGGGAGTAAACCCAGAGCAGAAAGACGTGTGCTTCTGCTGAGAC 3420  
Qy PheIleuSerSerThrArgPheAlaIleuSerIleuCysIleuAlaThrAlaAsnGlyIleuSer 1160  
Db 3421 TTCAAGAGCAGTACACGATTTGCCAGTCTCTGCTGCGGACAGGCAAAATGGTAGTCC 3480  
Qy GlnArgValAspAsnValGlnGlnIleSerSerProGlnIleProMetAlaGlyIleThrGlnHisIle 1180  
Db 3481 CAGAGAGTTGACAACTGGAGACAGACTCCCGGACCCAGAGCAGGAGGACGAGACACAA 3540  
Qy GlnAspIleuMetIleuSerValGlyIleThrSerGlyValAlaTrpSerGluThrAlaGlyIleuGln 1200  
Db 3541 CAAATTAATGTTGAGTGTGATTAATTCGGAAGCTGTGTGTAATCTGAGCTGACG 3600  
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Db 3601 GGGCTTGATCAACAGTGTGATCATGACCAAGAGGTATGGCTGTGCTAGGAGAG 3660  
Qy GluIleuSerSerArgGlyIleuCysProThrValIleuMetThrThrAlaValCysProGly 1240  
Db 3661 GAGCTGAGCTGAGGGGCTGTGTGTCAACAGTGTGATGACAGAGCGGTGTGTCTGTGT 3720  
Qy HisTrpGluArgLeuGlyIleSerArgGlyIleThrCysIleuAsnSerAlaAspAspHisSerGly 1260  
Db 3721 CACTGGAGCGGCTGGGCTCTAAGGGGCTGTGTCTTAACATGTCTGATGACACAGCGGT 3780  
Qy ValSerTrpSerLeuGlyAlaAlaGlyIleuGlnIleuValIleSerAsnSerAlaAspAsp 1280  
Db 3781 GTGTCTGTGTACTGGAGCGGCTGGGCTGAGGGGCTGTGTCCACAGTGTGATAC 3840  
Qy HisSerGlyValAlaIleTrpSerIleuGlyAlaAlaGlyIleuGlnIleuValIleSerAsnSer 1300  
Db 3841 CACAGCGGTGTGGCTGTGCTGAGAGCGGCTGGGCTGAGGGGCTGTGTCCAAACGT 3900  
Qy AlaAspAspHisSerGlyValIleSerTrpSerIleuGlyAlaAlaGlyIleuGlnIleuValIle 1320  
Db 3901 GCTATATACCAACAGCGGTGTGTCTGTGTCACTGGAGAGGCTGGAGCTGGAGAGGCTGTG 3960  
Qy SerAsnSerAlaAspAspHisSerGlyValIleSerTrpSerIleuGlyAlaAlaGlyIleuGln 1340  
Db 3961 TCACAACGTGTGATGACCAACAGCGGTGTGTCTGTGTCACTGGAGAGGCTGGAG 4020  
Qy GlyIleuValSer 1344  
Db 4021 GGGCTGTGTCT 4032

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RESULT 2
US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US2003002757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Blacher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 0734-34001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
US-10-066-521-5

Alignment Scores:
Pred. No.: 0 Length: 4035
Score: 7074.00 Matches: 1344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-066-521-5 (1-4035)

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DB 1 ATGGAAGAAGCAATCGCTCACCTTTCCAGTACGGGCTGCATGGTGCTCTATGAG 60
QY 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysSerSerGluSer 40
DB 61 CTAGACAGAGAAATTCAGACATTCAGAAATTAACAAAGAAATTCCTCAGAAATCG 120
QY 41 ThrThrCysSerTieProGlnPheGluLileGluAsnValLileGluCysLeuAlaLeu 60
DB 121 ACCCAATGCTTATTCACAGATTGAATCGAATGCGAATGCTGGCACTC 180
QY 61 LeuLeuHisGluTyrglyAlaSerLeuAlaTrrAlaThrSerTieSerTiePheGlu 80
DB 181 CTCCTGATGATGATTTATGAGCATCGCTGGCTGGGCTACGTCCATTAGCATTTGAA 240
QY 81 AsnMetAsnLeuAgtThrLeuSerGluLysAlaArgAspMetLysLysSerGln 100
DB 241 AACATGAACCTGCACACCTCTCGAAGAGCACGGATGACATGAAGAAATTCACAA 300
QY 101 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnLileSerGlnAla 120
DB 301 GCTATGAAACAAGAGGTGCACAGCACAGACAGAAAGAAATTCACAGCT 360
QY 121 MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnLileSerGlnAla 140
DB 361 ATGGAACAAGAGGTGCACAGCACAGACAGAAAGAAATTCAGAGCA 420
QY 141 TrpAspTyrglySerHisValMetThrLysPheAlaGluGluGluAspValArgArgSer 160
DB 421 TGGGACTACAGAGATGACGTGATGACCAATTCCTGAGGAGGAGTGTACGTGATGT 480
QY 161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSer 180
DB 481 TTGAAACACTGCTGCTGACGCGGAAATGCAACGTGGCTGGTCTTTGATTC 540
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QY 181 AspArgTrpGlyPheAspProArgThrValValLeuHisGlyLysSerGlyTieGlyLys 200
DB 541 GACCGGTGGGGCTTCCGGCTCGCACGGTGCTTCGACGGAAGTCAGAAATTCGAGAAA 600
QY 201 SerAlaLeuAlaArgArgTieValLeuCysTrpAlaGlnGlyGlyLeuTyrglnGlyMet 220
DB 601 TGGCTCTAGCCAAAGATGCTGCTGCTGGGCGCAAGGTGACTCTACAGAGCAATG 660
QY 221 PheSerTyrglyPhePheLeuProValArgGluMetGlnArgLysGluSerSerVal 240
DB 661 TTCCTACGCTCTTCTCTCTCCCGTTAGAGATGACAGGGAAGAAAGAGACAGTGC 720
QY 241 ThrGluPheTieSerArgGluTrpProAspSerGlnAlaProValThrGluTieMetSer 260
DB 721 ACAGATTCATCTCCAGAGGATGGCCAGACTCCACAGGCTCCGGTGAAGAGATCATGTCC 780
QY 261 ArgProGluArgLeuLeuPheTieTieAspGlyPheAspAspLeuGlySerValLeuAsn 280
DB 781 CGACCAAGAAAGCTGTGTTCATCATTCAGCGTTTCATATGACTGGGCTCTGTCTTAC 840
QY 281 AsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnProPheThrLeuTieArg 300
DB 841 AATGACACAAAGCTCTGCAAAAGACTGGGCTGAGAGACGCTCCGTTCACTTCATAGCC 900
QY 301 SerLeuLeuArgLysValLeuLeuProGluSerPheLeuTieValThrValArgAspVal 320
DB 901 AGTCTCGAGAGAGTCTGCTCTCCGAGCTCTCCGATCCGTCACCGTCAGAGACGTG 960
QY 321 GlyThrGluLysLeuLysSerGluValValSerProArgTyrglyLeuLeuValArgGlyTie 340
DB 961 GGCACAGAGAAAGCTCAAGTCAAGAGTGTGTCTCCGTTACCTGTAGTAGAGAAATC 1020
QY 341 SerGlyGluGlnArgTieTieLeuLeuLeuGluLysGlyTieGlyGluHisGlnLysThr 360
DB 1021 TCCGGGAACAAGAAATCCACTTGTCTCTTGAAGCGGGATGGTGAAGCATCAGAAACA 1080
QY 361 GlnGlyLeuArgAlaTieMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAla 380
DB 1081 CAAAGGTGGGTGGATCATGAAACAAACCGTAGCTGTCTCAACAGTCCAGGTGCCGCC 1140
QY 381 ValGlySerLeuTieCysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAla 400
DB 1141 GTGGCTCTCTCATCTGCTGCTGGCCCTGACCTGAGGACGTGGTGGAGAGGTGCGC 1200
QY 401 ProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrPro 420
DB 1201 CCTTCAACCAAGCTCACAGGCTGCAAGCCCTTTGTGTTCATCAGCTCACTCCCT 1260
QY 421 ArgGlyValValArgArgCysLeuAsnLeuGluGluValValLeuLysArgPheCys 440
DB 1261 CGAGGCTGTGCGCGCTGCTCTCAATCTGAGGAAAGATTTGCTCGAAGCGCTTCTGC 1320
QY 441 ArgMetAlaValGluGlyValTrrPheAsnArgLysSerValPheAspGlyAspAspLeuMet 460
DB 1321 GATATGGCTGTGAGGAGGTGGAATGGAAGTCATGTGTGATGGTGTGAGACATCATG 1380
QY 461 ValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnTieLeuLeuPro 480
DB 1381 GTTCAAGGACTCGGGAGGTGTGAGCTCCGTGCTCTGTTCATGATGACATCTTCTCCA 1440
QY 481 AspSerHisCysGluGluTyrglyTrpThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
DB 1441 GACAGCACTGTGAGGATGACTACACTTCTTCCACTCAGTCTCCAGAGCTTGTGGCC 1500
QY 501 AlaLeuTyrglyTrpValLeuGluGlyLeuGluTieGluProAlaLeuCysProLeuTyrglyVal 520
DB 1501 GCCCTGTACTACGCTGTAGAGGCTGTGAATGAGGCACTCTCTGCTGTACTGTT 1560
QY 521 GlyLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHisTieHisSerLeuTrp 540
DB 1561 GAGAGACAAAGAGTCAATGAGCTTAAACAGGCAAGCTTCCATATCCACTCGCTTTGG 1620
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QY 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560  
 Db 1621 ATGAAGCGTTTCTTGCTTGCTGCTGAGCGAAGCGTAAGAGGCCACTGGAGGTCCTG 1680  
 QY 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuHisTrpValSerLeuLeu 580  
 Db 1681 CTGGGCTCTCCCGTTCCTGGGGGTGAAGCAAGCTTCGACCTGGGCTCTCTCTGTTG 1740  
 QY 581 GLyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPhe 600  
 Db 1741 GGTCAAGCGCCCTAAATGCCACCCACAGAGACACCCCTGAGCGCTTCACCTGCTTTTC 1800  
 QY 601 GluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeu 620  
 Db 1801 GAGACTCAAGCAAGAGCTTTGTTGCTTGCTGGCATTTAAACAGCTTCAGAGAGTGGGCTT 1860  
 QY 621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640  
 Db 1861 CCGATTAAACAGAACCTGGACTTGATGACATCTTCCTGCTCCAGACACTGTCCTGAT 1920  
 QY 641 LeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAlaGluAla 660  
 Db 1921 TTGGCAAAATTCGGGTGATGTCAGAGGAGTCTTCCAGAGAGATCGGCTGAGGCA 1980  
 QY 661 CysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTrpLysAsp 680  
 Db 1981 TGTCTGTGTCCTCTATGATGCGGATGAAGACCTTCATTGAGAGACAGTGGGAAAT 2040  
 QY 681 PheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIle 700  
 Db 2041 TTCTGCTCCATGCTGGGACCCACCCACCTGCGGAGCTGAGACCTGGGAGCAGCAGATC 2100  
 QY 701 LeuThrGluValArgAlaMetLysThrLeuCysAlaLysValAspArgHisProThrCysLysIle 720  
 Db 2101 CTGACAGAGCGGGCCATAGAACCTGTGTGCCAAGCTGAGGCACTCCACCTGCAGAGTA 2160  
 QY 721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgIle 740  
 Db 2161 CAGACCCCTGATGTTTGAAGATGCAACAGATTACCTCGGTGTGACGACCTCTGGAGATC 2220  
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Db 3841 CACAGCGGTGTGGCTGTGTCTGACCTGGAGCGGCTGGGCTCGAGGGGCTTGTCACACAGT 3900  
Qy 1301 AlaApsApsHisserGIyValaIserTrpSerIeuGIyAlaIaIagIyeuGIuGIyLeuVal 1320  
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Db 4021 GGGCTGGGTCT 4032  
RESULT 3  
US-10-416-642-3  
; Sequence 3, Application US/10416642  
; Publication No. US20040043452A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: RANKUMAR, Jayalaxmi  
; APPLICANT: ARVIZU, Chandra  
; TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-0842 PCT  
; CURRENT APPLICATION NUMBER: US/10/416,642  
; CURRENT FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: 60/249,407  
; PRIOR FILING DATE: 2000-11-15  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 3489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1  
US-10-416-642-3  
Alignment Scores:  
Pred. No.: 0 Length: 3489  
Score: 5756.00 Matches: 1102  
Percent Similarity: 95.34% Conservative: 2  
Best Local Similarity: 95.16% Mismatches: 54  
Query Match: 81.37% Indels: 54  
Gaps: 1  
US-10-066-521-6 (1-1344) x US-10-416-642-3 (1-3489)  
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Qy 21 LeuApsIySGIuGIuPheGIuThrPheIySGIuLeuIySlySlySerSerGIuSer 40  
Db 61 CTAAACAAAGAAATTTCAACATTCAGAAATTAATTAAGAAATTTCTTCAAGATCG 120  
Qy 41 ThrTrpCySerIleProGIuPheGIuIleGIuAAsnAlaAAsnValGIuCySLeuAlaIeu 60  
Db 121 ACCACATGCTCTATTCCACAGTTTGAATCGAATCGCAACGTGGAATGTCTGGCACTC 180  
Qy 61 LeuLeuHisGIuTrpTrpGIyAlaIserIeuAlaItrpAlaItrpSerIleSerIlePheGIu 80  
Db 181 CTCTTGATGTAGTATTTAGAGCATCGCTGGCTGCGCTACATTAAGCATCTTTGAA 240  
Qy 81 AsnMetAAsnLeuArgTrpLeuSerGIuIyValaIArgApsApsMetIyS----- 96  
Db 241 AACATGAACCTGCGAACCTCTCGAGAAAGCGAGGATGACATGAATAATTTCACCAAGAA 300

Qy 96 ----- 96  
Db 301 GATCTGAAGCAACGATGACTGACCAAGACCAAGCAAGAAAAATGCCAGAAAAATAAA 360  
Qy 96 ----- 96  
Db 361 TATGCGATGACTTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTGGAATATAAACAC 420  
Qy 97 -----LysIleSerGIuAlaMetGIuGIuGIy 106  
Db 421 AAGTATGTGGAAATTCATTCCTTTTTCAGAAATTTTCACAGCTATGGAACAGAAAGT 480  
Qy 107 AlaThrAlaIaIagIuThrGIuGIuGIuGIuIleSerGIuAlaMetGIuGIuGIyAla 126  
Db 481 GCCACAGACAGACAGACAGAAACAAAGAAATTTCAACAGCTATGGAACAGAAAGTGGCC 540  
Qy 127 ThrAlaIaIagIuThrGIuGIuGIuGIuIleGIyValaIAspTrpTrpApyTrpIySerHis 146  
Db 541 ACAGACAGACAGACAGAAACAAAGACATGAGGTACACATGGACTACACAGATGTC 600  
Qy 147 ValMetThrIySPhenAlaGIuGIuGIuGIuAAspValaIArgTrpSerPheGIuAAsnThrAla 166  
Db 601 GTGATGACCAAAATTCGCTGAGAGAGAGAGATGATGCTGATGTTTGAACACCTGCTGCT 660  
Qy 167 AspTrpProGIuMetGIuThrLeuAlaGIyAlaPheApsSerApsApyTrpGIyPheArg 186  
Db 661 GACTGGCCGGAAAGCAACGTTGGCTGTGCTTTGATTTCAGACCGGTGGGCTTCGG 720  
Qy 187 ProArgThrValaIleuHisGIyIySerGIyIleGIyIySerAlaIeuAlaIArg 206  
Db 721 CTTGCAAGGTGTCTGACAGGAAAGTCAGAAATGGAATGGCTCTAGCAAGAGG 780  
Qy 207 IleValIeuCySTrpAlaGIuGIyIleuTrpGIuGIuMetPheSerTrpValaIlePhe 226  
Db 781 ATCGTGTGTGTCTGGGGCAAGTGAAGTCACTACACAGGAATGTTCTCTACGTCTTCTTC 840  
Qy 227 LeuProValaIArgIuMetGIuArgIyLeuGIuSerSerValaIArgIuPheIleSerArg 246  
Db 841 CTCCCGCTTGAAGAGATGACGCGGAAAGAGAGAGATGTCACAGAGTTTCATCTCCAGG 900  
Qy 247 GIuTrpProApsSerGIuAlaProValaIleuGIuIleMetSerApyProGIuArgLeuIeu 266  
Db 901 GAGTGGCCAGACTCCAGGCTCGGTGACGAGATCATGTCCGACCAAGAAAGCTGTGG 960  
Qy 267 PheIleIleApsGIyPheApsApsIeuGIySerValaIleuAAsnAAsnApyTrpIyLeuCyS 286  
Db 961 TTTCACTATGACGTTTTCAGATGACTGGGCTGTCTCTCAACATGACACAAAGCTTGC 1020  
Qy 287 LysApyTrpAlaGIuIySGIuProProPheThrIeuIleArgSerIeuLeuArgIyVal 306  
Db 1021 AAAGACTGGGCTGAGAGACAGCTCCGTTCACTCATACGAGTGTGTGAGAGAGGTC 1080  
Qy 307 LeuIeuProGIuSerPheIeuIleValaIArgApyValaIArgIuIyLeuIyS 326  
Db 1081 CTGCTCTCTGAGTCTTCTGATGTCAACGTCAGAACGTGGGCAACAGAACTCAAG 1140  
Qy 327 SerGIuValaIleSerProArgTrpLeuIeuValaIArgIyIleSerGIyGIuGIuArgIle 346  
Db 1141 TCAGAGGTGTGTCTCCCGTTACTCTTGTAGAGAAATCTCCGGGAAACAAAGATC 1200  
Qy 347 HisLeuIeuIeuGIuArgGIyIleGIuIleHisGIuIyArgIuGIuIyLeuArgAlaIle 366  
Db 1201 CACTTGCTCTTGAGCCGGGATTTGGAGCATCAGAAAGACACAAAGGTTGGCGCATC 1260  
Qy 367 MetAAsnAAsnArgIuLeuIeuApsGIuCyGIuValaIProAlaValaIleGIySerIleIleCyS 386  
Db 1261 ATGAACAACGTTGAGCTGTCAACAGTGCACAGGTGCCCGCGGTGCTCTCATCTGC 1320  
Qy 387 ValaIleuGIuIeuGIuAAspValaIleGIuIySerValaIleProPheAAsnGIuThrLeu 406  
Db 1321 GTGGCTCTGACGTGCGAGAGATGTGTGGGAGAGAGCTGCCCTCTTCAACCAACGCTC 1380  
Qy 407 ThrGIyLeuHisAlaIlePheValaIleHisGIuIleuThrProArgGIyValaIArgArg 426

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Db      1381  ACAGGCGCGACGCGCTTTGTGTTTCATGAGCTCACCCCTCGAGGGGTGGTCCGGGCG 1440
Qy      427  CysleuamleuGluGluArgValValleuYsaArgPheCy8ArgMetAlaValGluGly 446
Db      1441  TGTCTCAATCTGGAGAAAGAGTGTCTCTGAGAGCCCTTCTGCGATGCGTGGAGGGA 1500
Qy      447  ValTrrAsnArgLysSerValPheAspGlyAspAspLeuMetValGluGlyGlu 466
Db      1501  GTTGGAATAGGAATGACGTGTTTACACGTTGACACCTTCATGTTCAAGAGCTCGGGAG 1560
Qy      467  SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGlu 486
Db      1561  TCTAGGCTCCGTCGCTGTTTCAATGAACATCTTCTCCAGACAGCCATGTAAGAGAG 1620
Qy      487  TyrTrrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeu 506
Db      1621  TACTAACACCTTCTTCCACCTCAGTCTCCAGAGCTTCTGCGCGCTTGTACTACGTGTTA 1680
Qy      507  GluGlyLeuGluGluIleGluProAlaLeuCysProLeuTyrValGluYsaThrLysArgSer 526
Db      1681  GAGGCGCTGGAAATCGAGCCAGCTCTCTGCGCTGTGACGTTGAGAAACAAAGAGGTCC 1740
Qy      527  MetGluLeuYsaGlnAlaGlyPheHisAlaHisSerLeuTyrMetLysArgPheLeuPhe 546
Db      1741  ATGAGAGCTTAACAGGAGGCGCTTCATTCACCTGCTTGGATGAAGCGTTTCTGTTT 1800
Qy      547  GlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValPro 566
Db      1801  GGCCTCGTGAACGAAAGAGTAAAGAGGCGCACGTGAGGTCTGCGGGCTGTCGCCCTTCC 1860
Qy      567  LeuGlyValLysGlnLysLeuLeuHisTrrValSerLeuLeuGluGlnGlnProAsnAla 586
Db      1861  CTGGGGGTGAAGAGAGAGCTTCTGACATGGGCTCTCTGTTGGGTCACAGCTAATATCC 1920
Qy      587  ThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGlu 606
Db      1921  ACCAGCCCGAGAGACACCTTGAGCGCTTCCATGCTCTTTCGAGAGCTCAAGACAAAGAG 1980
Qy      607  PheValArgLeuAlaLeuAsnSerPheGlnGluValTrrLeuProIleAsnGlnAsnLeu 626
Db      1981  TTTGTTCGCTTGGCATTTAAACAGCTTCCAAAGAGTGTGCTTCCATTAACACAGAACCTG 2040
Qy      627  AspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgVal 646
Db      2041  GACTGTAAAGATCTCTCTGCTCCAGACATGTCGTAATTTGCGGAAATTCGGGGTGG 2100
Qy      647  AspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValProLeu 666
Db      2101  GATGTCAAAAGGAGCTTCCCAAGAGATGATCCGCTGAGGCAATGCTGTGGTCCCTCTA 2160
Qy      667  TrpMetArgAspLysThrLeuIleGluGluGlnTrrGluAspPheCysSerMetLeuGly 686
Db      2161  TGGATGGCGGATTAAGACCCCTCATTTAGGAGAGATGGGAAAGATTCTGCTCATGCTTGGC 2220
Qy      687  ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706
Db      2221  ACCACACCAACACCTGGCGGACCTGACCTGGCGAGACATCTCGACAGACGGGCGCATG 2280
Qy      707  LysThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArg 726
Db      2281  AAGAGCCCTGTGTGCGCAAGCTAGGCAATCCACCTGCAAGATACAGACCTTAATGTTTGA 2340
Qy      727  AsnAlaGlnIleThrProGlyValGlnHisLeuTrrArgIleValMetAlaAsnArgAsn 746
Db      2341  AATGACACAGATTACCCCTGATGTGACAGCACTTGGAGAAATCGTCAATGGCCAAACGTAAC 2400
Qy      747  LeuArgSerLeuAsnLeuGlyGlyThrHisLeuYsaGluGluAspValArgMetAlaLys 766
Db      2401  CTAAGATCCCTCAACTGGAGGCGACCCACCTGAAGAGAGATGAAGATGGCGGT 2460
Qy      767  GluAlaLeuYsaHisProLysCysLeuLeuGluSerLeuArgLeuAspCysGlyLeu 786

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Db      2461  GAAGCTTTAAACACCCAAATGTTTGTGAGATCTTTAGAGCTGAGATTGCTGTGATG 2520
Qy      787  ThrHisAlaCysTrrLeuValIleSerGlnIleLeuThrThrSerProSerLeuYsaSer 806
Db      2521  ACCAGTCCCTGTATCTGAAGATCTCCAAATCTCTTACGACCTCCCAAGCTGAAATCT 2580
Qy      807  LeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeu 826
Db      2581  CTGAGCTGGCAGGAAACAGAGTGAACAGACAGGAGATTAAGCTCTCAGTGAATGCTTGG 2640
Qy      827  ArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThr 846
Db      2641  AGAGTCTCCAGTGGCGCTTCAGAAAGCTGAATCTGAGAGACTGTGGCATACACACAGC 2700
Qy      847  GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
Db      2701  GATTGCCAGATCTGGGCTTCAAGCCCTGTCAGCAACCGAGCTTGAACACCTGTGGCTTA 2760
Qy      867  SerAsnAsnSerLeuGluYsaGlnGlyValAlaAsnLeuLeuCysArgSerMetArgLeuPro 886
Db      2761  TCCAAACACAGCTGGGGAACGAGGTGTAAATCTACTGTGTCAATGATGAGGCTTCC 2820
Qy      887  HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
Db      2821  CACTGTAGTCTGACAGAGCTGATGCTGAATCAGTCCACCTGGACACCGCTGGCTGTGGT 2880
Qy      907  PheLeuAlaLeuAlaLeuMetGlyAsnSerTrrLeuThrHisLeuSerLeuSerMetAsn 926
Db      2881  TTTCTTGACCTTGGCTTATGTTATGTTAATCTCAAGGCTGAGACCTGAGCTTAAGCATGAAAC 2940
Qy      927  ProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgLysProSerCysHis 946
Db      2941  CCTGTGAAGACATATGGCGTAACTTGTGCGAGGTCATGAGAGACATCTTGTTCAT 3000
Qy      947  LeuGlnAspLeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSer 966
Db      3001  CTCGAGAGCTGAGATTGTAAAGTTCATCTCACCGCGCGTGTGAGAGATCTGTGCC 3060
Qy      967  CysValIleSerArgSerArgHisLeuLysSerLeuAspLeuTrrAspAsnAlaLeuGly 986
Db      3061  TGTGTGATCTGAGAGAGACACCTGAAGAGCTGGAATCTCAAGACATATGCCCTGGGT 3120
Qy      987  AspGlyGlyValAlaAlaLeuCysGluGlyLeuYsaGlnLysAsnSerValLeuThrArg 1006
Db      3121  GACGCTGGGTTGCTGTGACCTGTGCGAGGAGCTGAAGACAAAGACATGTTCTGACAGAG 3180
Qy      1007  LeuGlyLeuYsaAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeu 1026
Db      3181  CTCGGGTGAAGGCAATGAGACTGATCTTGAATGCTGTGAGGCACTCTCTTGGCCCTT 3240
Qy      1027  SerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db      3241  TCTGCAACCCGCACTGACCAAGCTTAACCTGTGTGCGAATTAATTCAAGTCCCAAGAG 3300
Qy      1047  MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeu 1066
Db      3301  ATGATGAAGCTGTGTGGCTTGTGCTTGTCCAGCTTCACTTAACAGATTAATTTGGGCTG 3360
Qy      1067  TrpLysTrrGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuYsa 1086
Db      3361  TGGAAATGGCAGTACCCGTGTCAATTAAGAAAGCTGTGGAGGAAAGTCACTACTCAAG 3420
Qy      1087  ProArgValValIleAspGlySerTrrHisSerPheAspGluAspAspArgHis 1104
Db      3421  CCCCGAGTCTGAATTAAGACGTAATGGCATTTCTTATGAATGAACCCGGTAC 3474

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## RESULT 4

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US-10-216-645-1
; Sequence 1, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LBSL, MONIKA

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; APPLICANT: PETERS-KOTTIG, MICHAEL
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; PRIORITY FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 3926
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-216-645-1

Alignment Scores:
Pred. No.: 0 Length: 3926
Score: 5756.00 Matches: 1102
Percent Similarity: 95.34% Conservative: 2
Best Local Similarity: 95.16% Mismatches: 0
Query Match: 81.37% Indels: 54
DB: 15 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-216-645-1 (1-3926)

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Db 1 ATGAGAAGAGCAAAATGGCTCACCTTTCCAGCTACGGGCTGCATGGTGTCTCTAGAG 60

Qy 21 LeuAspLysGluLysPheGlnThrPheLysGluLeuLysLysLysSerSerGluSer 40
Db 61 CTACACAGAGAGAAATTCACACATTCAGAAATTAAGAAATCTTCAGAAATCG 120

Qy 41 ThrThrCysSerTleProGlnPheGluLysGluLysLysLysLysLysLysLysLys 60
Db 121 ACCCAAGCTCTATTCACAGTTTGAAATCGAAGATCGCAAGATGCTGGCACTC 180

Qy 61 LeuLeuHisGluLysTyrglyLysLysLysLysLysLysLysLysLysLysLysLys 80
Db 181 CTCCTGGATGAGTATTATGAGCATCGCTGGCTGGCTGCTGCTGCTGCTGCTGCTG 240

Qy 81 AsnMetAsnLeuAspGlyThrLeuSerGluLysLysLysLysLysLysLysLysLys 96
Db 241 AACATGAACCTCGCAACCTCTCGAGAGAGCAGCGATGACATGAATAATTCACAG 300

Qy 96 ----- 96
Db 301 GATCTGAGCAAGCATGATGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 360

Qy 96 ----- 96
Db 361 TATGGCATGACTAAGCTTATCTTGGGGTGTCTGACATCTCTGACTGCAATATAAC 420

Qy 97 -----LysIleSerGlnIleMetGluGlnGluGly 106
Db 421 AAGTATGTGGAAATTCATCTTCTTTTGCAGAAATTCACAACTATGCAAGCAAGAG 480

Qy 107 AlaThrAlaIleGluThrGluGluGluGluLysSerGlnIleMetGluGlnGluGly 126
Db 481 GCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

Qy 127 ThrAlaIleGluThrGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 146
Db 541 ACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

Qy 147 ValMetThrLysPheAlaGluGluGluGluGluGluGluGluGluGluGluGluGlu 166
Db 601 GTGATGACCAAAATTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

Qy 167 AspTrpProGluMetGlnThrLeuAlaGluLysPheSerSerAspArgTrpGlyPhe 186
Db 661 GACTGGCCGGAAGCAAGCGTGGCTGGTCTTTTGAATTCAGACCGGTGGGGCTTCCGG 720
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Qy 187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 206
Db 721 CCTGCACGGGTGGTTCGACAGGAAGTCAAGAAATCGGCTTACAGCAGAGAG 780

Qy 207 IleValLeuCysTrpAlaGlnGlyGlyLeuTyrgluGlnLysPheSerTyrglyPhe 226
Db 781 ATCGTGTGTGTGGGGGCAAGGTGAGCTTACAGAGGAATGTTCTCTAGCTTCTTC 840

Qy 227 LeuProValArgGluMetGlnArgLysLysGluLysSerSerValThrGluPheIleSer 246
Db 841 CTCCCTTTAGAGAGATCGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

Qy 247 GluTrpProAspSerGlnAlaProValThrGluLysSerArgProGluArgLeu 266
Db 901 GAGTGGCCAGACTCCAGGCTCCGGTGACGGAAGATCATGTCCGACAGAAAGCTGTG 960

Qy 267 PheIleIleLeuArgLysPheAspAspLysLysSerValLeuAsnAsnAspThrLys 286
Db 961 TTCATCATTTGACGGTTTCGATGACCTGGCTGTGTCTTCAACAATGACACAAACCT 1020

Qy 287 LysAspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgVal 306
Db 1021 AAAGACTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080

Qy 307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLys 326
Db 1081 CTGCTCCCTGAGTCTTCTGATGCTCACCGTCAGAGAGAGAGAGAGAGAGAGAGAG 1140

Qy 327 SerGluValValSerProArgTyrglyLeuValArgLysLysSerGlyGluGlnArg 346
Db 1141 TCAGAGGTGTGTCTCCCGTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200

Qy 347 HisLeuLeuLeuGluArgGlyIleGlyLysLysLysLysLysLysLysLysLys 366
Db 1201 CACTGCTCTTGAAGCCGGGATTTGGTGAACATCAAGAGAGAGAGAGAGAGAGAG 1260

Qy 367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIle 386
Db 1261 ATGAACAACCGTAGCTGTGCACAGTGCAGAGTGCAGAGAGAGAGAGAGAGAGAG 1320

Qy 387 ValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThr 406
Db 1321 GTGGCCCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380

Qy 407 ThrGlyLeuHisAlaIlePheValPheHisGluLeuThrProArgGlyValAlaArg 426
Db 1381 ACAGGCTTGACCGCGCTTTTGTGTTCATCATGCTCACCCCTGAGGCGTGTCCGG 1440

Qy 427 CysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGly 446
Db 1441 TGTCTCAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500

Qy 447 ValTrpAsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGly 466
Db 1501 GTGTGAATGTGAAGTGAAGTGTGTGAAGTGAAGTGTGTGAAGTGTGTGAAGTGT 1560

Qy 467 SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGlu 486
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Qy 487 TyrTyThrPhePheHisLeuSerLeuGlnAspPheCysAlaIleLeuTyrglyVal 506
Db 1621 TACTACACCTTCTTCCACTCAAGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680

Qy 507 GluGlyLeuGluLysGluProAlaLeuCysProLeuTyrglyGlyThrLysArgSer 526
Db 1681 GAGGAGCTGGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740

Qy 527 MetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuThrPheLysArgPheLeu 546
Db 1741 ATGAGGCTTAAACAGGAGGCTTCCATATCATCTGCTTGGAGTGAAGAGCGTTTGT 1800
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QY 547 G1yleuValSerGluAspValArgArgProLeuGluValLeuLeuGluCysProValPro 566  
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 QY 567 LeuGluValIlyGlnIlyLeuLeuH1sTrpValSerLeuLeuGluGlnProAsnAla 586  
 Db 1861 CTGGGGGAGAGCAAGAGCTTCTGCACTGGGCTCTCTGGTGGGCTCACAGCTTAATCC 1920  
 QY 587 ThrThrProGluYAspThrLeuAspAlaPheH1sCysLeuPheGluThrGluAspIlyGlu 606  
 Db 1921 ACCACCCGAGAGAGACCCCTGAGCCCTTCCACTGCTTTTTCGAGACTCAAGACAAAG 1980  
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 Db 1981 TTTGTTCCCTTGGCATTAACAGCTTCCAGAGAGTGGCTTCCGATTAACAGAACTG 2040  
 QY 627 AspleuIleAlaSerSerPheCysLeuGlnH1sCysProIlyLeuArgIlyIleArgVal 646  
 Db 2041 GACTTGATAGCATCTTCTTCTGCTCCAGCACTGCTCGTATTTGCGAAATTCGGGTG 2100  
 QY 647 AspValIlySerGluIlePheProArgAspGluSerAlaGluAlaCysProValValProLeu 666  
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 QY 707 LysThrLeuCysValAlaLeuLeuArgH1sProThrCysIlyIleGlnThrLeuMetPheArg 726  
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 QY 787 ThrH1sAlaCysIlyTrpLeuIlyIleSerGlnIleLeuThrTrpSerProSerLeuYser 806  
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 QY 807 LeuSerLeuAlaGluYasnIlyValThrAspGlnIlyValMetProLeuSerAspAlaLeu 826  
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 Db 3301 ATGATGAAGCTGTGTTCGGCTTGTGCTTGTCCAGCTTAATTAACATTAATTTGGGTG 3360  
 QY 1067 TrpLysTrpGlnIlyProValGlnIleArgIlyLeuLeuGluGluValGlnLeuLeuIly 1086  
 Db 3361 TGGAAATGGAGTAACTCTGTCAATTAAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAG 3420  
 QY 1087 ProArgValValIleAspGlySerTrpH1sSerPheAspGluAspAspArgH1s 1104  
 Db 3421 CCCCAGAGTGTAAATGAAGGATTTGGCATCTTTTATGAAGATGAACCGGTAC 3474

RESULT 5  
 US-10-860-761-3  
 ; Sequence 3, Application US/10860761  
 ; Publication No. US2004024875A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MYETH  
 ; TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS  
 ; FILE REFERENCE: AM101318  
 ; CURRENT APPLICATION NUMBER: US/10/860,761  
 ; CURRENT FILING DATE: 2004-06-03  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 3  
 ; LENGTH: 3885  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3603)  
 US-10-860-761-3

Alignment Scores:  
 Pred. No.: 0 Length: 3885  
 Score: 5741.50 Matches: 1098  
 Percent Similarity: 96.16% Conservative: 3  
 Best Local Similarity: 95.90% Mismatches: 3  
 Query Match: 81.16% Indels: 41  
 DB: 18 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-860-761-3 (1-3885)  
 QY 1 MetGluGluAspIlySerLeuThrPheSerSerTrpGluLeuGlnTrpCysLeuIlyGlu 20  
 Db 154 ATGAGAGAGAGCAATGCTCACTTTTCCAGTACAGGAGCTGCAATGGTGTCTATGAG 213



QY 21 LeuaplysglupheglnthPhelysgluleuilylylseserSerGluSer 40  
 Db 214 CTAGACAAGAGAAATTCAGACATTCAGAGAAATTAAGAAATCTTCAGAAATCG 273  
 QY 41 ThrThrCysSerIleProGlnPheGlnIleGlnAsnValIleGluCysLeuAlaLeu 60  
 Db 274 ACCACATGCTATTTCACAGATTGAAATCCAAAGATCCAAAGATGTCGCACTC 333  
 QY 61 LeuLeuHlsGluYrTYrGlyAlaSerLeuAlaTPrAlaThrSerIleSerIlePheGlu 80  
 Db 334 CTCTTGATGATGATATATAGAGATCGCTGGCTGGGCTACGTCATTAAGCATTTGAA 393  
 QY 81 AsnMetAsnLeuAlaGlnThrLeuSerGluValAlaArgAspMetIlylys----- 97  
 Db 394 AACATGAACCTGCAGAACCTCTCGAGAGAGGACAGGATGACATGAAAGACATTCACCA 453  
 QY 97 ----- 97  
 Db 454 GAAGATCCTGAAGCAAGATGACCTGACCAAGAACCAAGAAAGAAAGTCCAGAAATT 513  
 QY 98 -----IleSer 99  
 Db 514 TCACAGCTGTGCAACAAGATAGTCCACAGCTGCAGAGACAAAGAAAGAACAGAAATTTCA 573  
 QY 100 GlnAlaMetGluGluGluGlyAlaThrAlaAlaGluThrGluGluGlnIleSerGln 119  
 Db 574 CAACGCTATGAAACAAGAGGTGCACAGACAGACAGACAGAAAGAAATTTCAAA 633  
 QY 120 AlaMetGluGluGluGlyAlaThrAlaAlaGluThrGluGluGluGlnIleGlyAlaAsp 139  
 Db 634 GCTATGGAACAAGAGGTGCACAGACAGACAGACAGAAAGAAAGACATGAGAGGTAC 693  
 QY 140 ThrTrpAspTYrLYsSerHlsValMetThrLYsPheAlaGluGluGluAspValArgArg 159  
 Db 694 ACATGGGACCTACAAAGATCAAGTATGACAAATTCGCTGAGAGAGAGATGACGTCT 753  
 QY 160 SerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAsp 179  
 Db 754 AGTTTGAACAACCTGCTGCTGACGCGCGGAAATGCAACGTTGCGTGTTCAT 813  
 QY 180 SerAspArgTrpGluPheArgProArgThrValValLeuHlsGlyLYsSerGlyIleGly 199  
 Db 814 TCACACGAGGTGCTCGGCTCGACAGGTGGTTCGACGGAAGTCAAGAAATTTGG 873  
 QY 200 LYsSerAlaLeuAlaArgArgIleValLeuCysTrpAlaGlnGlyLYsLeuTYrGlnGly 219  
 Db 874 AAATCGGCTACAGAGAGATGCTGTGCTGGCGCAAGGTGACCTTACCAAGGA 933  
 QY 220 MetPheSerTYrValPhePheLeuProValArgGluMetGlnArgLYsLYsGluSerSer 239  
 Db 934 ATGTTCTCTCAAGCTCTTCTCTCCCGTTAGAGATGACAGCGGAAGAGAGAGCAGT 993  
 QY 240 ValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet 259  
 Db 994 GTCAAGAGTTCATCTCGAGAGGTGGCAGACCTCCAGGCTCGGTGACAGAAATCATG 1053  
 QY 260 SerArgProGluArgLeuPheIleIleAspGlyPheAspPheGluSerValLeu 279  
 Db 1054 TCCCGACCAAGAAAGCTGTTGTTCACTTACACGTTTCATGACCTGGGCTCTGTCTC 1113  
 QY 280 AsnAsnAspThrLYsLeuCysLYsAspTrpAlaGluLYsGlnProProPheThrLeuIle 299  
 Db 1114 AACATGACACAAAGCTCTGCAAGACTGGCTGAAAGCAGCCTCCGTTCACTCATTA 1173  
 QY 300 ArgSerLeuLeuAlaGlyValLeuLeuProGluSerPheLeuIleValThrValArgAsp 319  
 Db 1174 CGCAGTCTGTGAGAGAGTCTCTCTCTGATGCTTCTGATCGTCAACGTCAGAGAC 1233  
 QY 320 ValGlyThrGluLYsLeuLYsSerGlyValValSerProArgTYrLeuLeuValArgGly 339  
 Db 1234 GTGGGACAGAGAGCTCAAGTCAAGAGTCTGTCTCTCCCTTACCTGTTAGTTAGAGA 1293

QY 340 IleSerGlyGluGlnArgIleHlsIleLeuLeuGluValArgLYsIleGlyGlnHlsGlnLYs 359  
 Db 1294 ATCTCCGGGAAACAAGAAATTCATTGCTCTTGAAGCGAGATGGTGGACATCAAG 1353  
 QY 360 ThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValPro 379  
 Db 1354 ACACAAAGGTGCTGCGGATCATCAACACCGTGAAGTCTTCAACAGTCCAGGTGCC 1413  
 QY 380 AlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValValGlyGluSerVal 399  
 Db 1414 GCCGTGGCTCTCATCTCGTGGCTGACCTGACGTGACAGACGTTGGGGAGAGCGTC 1473  
 QY 400 AlaProPheAsnGlnThrLeuThrGluLeuHlsAlaAlaPheValPheHlsGlnLeuThr 419  
 Db 1474 GCCCTTCAACCAAGCTCACAGGCTGACGGCTGACGGCTTGTGGCTTCAATCACTACC 1533  
 QY 420 ProArgGlyValValArgArgCysLeuAsnLeuGluGluValArgValValLeuLYsArgPhe 439  
 Db 1534 CTTGAGCGGTGTCCGGCTGTCTCAATCTGAGAAAGATTTGCTGMAAGCTTTC 1593  
 QY 440 CysArgMetAlaValGluGlyValTrpAsnArgLYsSerValPheAspGlyAspAspLeu 459  
 Db 1594 TGCGTATGCTGTGAGAGGATGTGAATAGAAATGCAAGTGTGATGTGACACCTC 1653  
 QY 460 MetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHlsMetAsnIleLeuLeu 479  
 Db 1654 ATGGTTCAAGACCTCGGAGAGTCAAGCTCGGTCTGTGTTCAATGAACATCTTCTC 1713  
 QY 480 ProAspSerHlsCysGluGluTYrTYrTYrThrPhePheHlsLeuSerLeuGlnAspPheCys 499  
 Db 1714 CCAACAGCACTGTGAGAGTACTACCTTCTTCACTTCACTTCACTTCACTTCACTTCTGT 1773  
 QY 500 AlaAlaLeuTYrTYrValLeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTYr 519  
 Db 1774 GCGCTTGTACTACGTTAGAGAGGCTGGAATCAGACAGCTCTGCTGCTGTAC 1833  
 QY 520 ValGluLYsThrLYsAspSerMetGluLeuLYsGlnAlaGlyPheHlsIleHlsSerLeu 539  
 Db 1834 GTTGAGAAACAAGAGTCAATGAACTTAAACAAGCAGCTTCAATATCCACTGCTT 1893  
 QY 540 TrpMetLYsArgPheLeuPheGlyLeuValSerGlyAspValArgArgProLeuGluVal 559  
 Db 1894 TGAATGAGCTTCTTCTTGTGGCTGTGAGCAAGACCTTAAAGAGGCCATGGAAGTTC 1953  
 QY 560 LeuLeuGlyCysProValProLeuGlyValLYsGlnLYsLeuLeuHlsTrpValSerLeu 579  
 Db 1954 CTGCTGGGCTGTCCCGTTCCCGTGGGGGTGAAGACAGATCTTGCACCTGGGTCTCTG 2013  
 QY 580 LeuGlyGlnGlnProAlaAlaThrThrProGlyAspThrLeuAspAlaPheHlsCysLeu 599  
 Db 2014 TTGGGTCAAGACCTAATGCAACACCCAGAGACACCTTGACCGCTTCCACTGTCTT 2073  
 QY 600 PheGluThrGlnAspLYsGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrp 619  
 Db 2074 TTCAAGCTCAAGACAAAGATTTGTTGCTTGGCATTTAAACAGCTTCCAAAGATGTGG 2133  
 QY 620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHlsCysPro 639  
 Db 2134 CTTCGATTAACCAAGACCTGGAATGATGACATCTTCTTGGCTCCAGACCTGTCCG 2193  
 QY 640 TYrLeuArgLYsIleArgValAspValLYsGlyIlePheProArgArgGluSerAlaGlu 659  
 Db 2194 TATTTGGGAAAAATTCGGGTGATGTCCAAAGGATCTTCCCAAGATGATGTGCGCTGAG 2253  
 QY 660 AlaCysProValValProLeuTrpMetArgAspLYsThrLeuIleGluGluGlnTrpGlu 679  
 Db 2254 GCATGCTGTGGTCCCTCTATGATGCGGGAATGAAGCCTCAATGAGAGACGTGGAAA 2313  
 QY 680 AspPheCysSerMetLeuGlyTYrHlsAspProHlsIleuArgGlnLeuAspLeuGlySerSer 699  
 Db 2314 GATTTTGTCTCATGCTGTGGACCCACCCACACTGTGGGACGCTGGGAGAGACG 2373  
 QY 700 IleLeuThrGluValMetLYsThrLeuCysAlaLYsLeuArgHlsProThrCysLYs 719

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Db      2274 ATCTGACAGAGCGGGCATGAAAGACCTGTGTGCAAGCTGAGGACATCCCACTGCAAG 2433
Qy      720  ILeGInThrLeuMetPheArgAsnAlaGlnIleThrProGlyValAlaGlnIleuThrArg 739
Db      2434 ATACGAGACCTCGATGTTTGAAGATGACAGATATCCCTGTGTGCAACACTCTGAGGA 2493
Qy      740  ILeValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrIleuArgGlu 759
Db      2494 ATCTGATGCGCCACCTGATTAAGATCCCTCAACTTGGAGGACCCCACTGAAAGAA 2553
Qy      760  GluAspValArgMetAlaCysGlnAlaLeuIleuArgIleuProIleuValLeuLeuSerLeu 779
Db      2554 GAGATGTAAAGATGCGGTGTGAACCTTAAACACCCAAATGTTGTGTGAGCTTTG 2613
Qy      780  ArgLeuAspArgCysGlyLeuThrIleuAlaCysGlyLeuIleuValIleSerGlnIleuThr 799
Db      2614 AGGCTGATGCTGTGATGATGACCATGCTGTATACCTGAAGATCTCCAAATCTTACG 2673
Qy      800  ThrSerProSerLeuLeuSerLeuSerLeuAlaGlyAlaAsnValIleThrAspGlnIleVal 819
Db      2674 ACCTGCCCAAGCTGAAATCTGTAGCTGTGCAAGAAACAGGTACAGACCAAGGAGTA 2733
Qy      820  MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnIleuIleuGlu 839
Db      2734 ACGCTCTCAGTATGCTGTGAGGGTCTCCAGTGCCTGCAAGCTGATATCTGAG 2793
Qy      840  AspCysGlyIleThrAlaIleThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db      2794 GACTGTGCATCATCAGCCAGCGGTGCGCAGTCTGAGCTCAGCCCTGTCAGCAACCGG 2853
Qy      860  SerLeuThrIleuValLeuSerAsnAsnSerLeuGlyAlaGlnGlyValAsnLeuLeu 879
Db      2854 AGCTTGACACCTGTGCTTATCCAAACAGCTTGGGAAACAGAGGTGTAATTTACTG 2913
Qy      880  CysArgSerMetArgLeuProIleCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db      2914 TGTGATCATGAGGCTTCCCACTGTATGTCTGCAAGAGGCTGATCTGATCAGGCCAC 2973
Qy      900  LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThr 919
Db      2974 CTGACACGCGCTGTGTGTTCTTCTTCACTTGTGCTTAAATGGGTAACTCATGCTGAGC 3033
Qy      920  HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIleValLeuLeuCysGlnVal 939
Db      3034 CACCTGAGCTTAGATAACTCTGTGAAGACATGCGTGAAGCTTCTGTGCGAGGTC 3093
Qy      940  MetArgGluProSerCysHisLeuGlnAspLeuGluLeuValIleCysHisIleuThrAla 959
Db      3094 ATGAGAGAACATCTTGTCACTCCAGACCTTGAAGTTGTTAACTGTCATCTCACCCC 3153
Qy      960  AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisIleuIleuSerLeuAsp 979
Db      3154 GCGGTCTGTGAGAGCTGTCTCTGTGTGATCTCGAAGACAGACACTGAAGAGCTTGAT 3213
Qy      980  LeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnGlyLeuIleuGln 999
Db      3214 CTCACGAGCAATGCTCGGTGAGCGGTGGGTGTGTGCTGTGTGAGAGGACTGAAGCA 3273
Qy      1000  LysAsnSerValIleuThrArgLeuGlyLeuIleuValIleCysGlyLeuThrSerAspCys 1019
Db      3274 AAGAACTGTTCTTCAAGACACTCGGCTTGAAGGATGTGACTGACTTCTGATTTGCTGT 3333
Qy      3334 GAGGCACTCTCTTGCCCTTTCCTGCAACCGGCACTGACCAAGCTTAACTCGGTGAG 3393
Qy      1040  AsnAsnPheSerProIleGlyMetMetIleuCysSerAlaPheAlaCysProThrSer 1059
Db      3394 AATACTTCAGTCTCCAAAGAAATGATGAGCTGTGTGCTTGTGCTGCTGCCAGCT 3453
Qy      1060  AsnLeuGlnIleIleGlyLeuTrpIleTrpGlnIleProValGlnIleArgIleuLeu 1079

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Db      3454 AACTTACAGATTAATTGGCTGTGAAATGCAATGCAATCCCTGTGCAATTAAGAACTGCTG 3513
Qy      1080  GluGluValGlnIleuLeuIleuProArgValIleLeaAspGlySerTrpHisSerPheAsp 1099
Db      3514 GAGGAGTGCAGCTTACTTAAGCCCGAGTCTTAATTGACGTAGTGGCATTTCTTTGAT 3573
Qy      1100  GluAspAspArgHis 1104
Db      3574 GAAGATGACCGGTAC 3588

RESULT 6
US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US2004002669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 5741.50 Matches: 1098
Percent Similarity: 56.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
DB: 17 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-399-443-23 (1-3900)
Qy      1  MetGluGlyAspIleuSerLeuThrPheSerSerTrpGlyLeuGlnTrpCysLeuTrpGlu 20
Db      154  ATGAGAGGAGCAATATGCTCACCCTTTCCAGCTTACGCGGCTGCAATGTGTCTATGAG 213
Qy      21  LeuAspIleuGluIleuPheGlnThrPheIleuGluLeuLeuGlyIleuSerSerGluSer 40
Db      214  CTAGCAAGAGAAATTCAGACATTCAGAGAAATTAAGAGAAATTCAGAGAAATTCAGAAATCG 273
Qy      41  ThrThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
Db      274  ACCACATGCTCTATTCACAGATTTGAATGCAAGATGCAACGATGCAATGTGTGCACTTC 333
Qy      61  LeuLeuHisGluTrpTrpGlyAlaSerLeuAlaTrpAlaTrpSerIleSerIlePheGlu 80
Db      334  CTCTTGATGATGATTAATGAGCATGCGTGTGCTGCGGTACATGATCATTAGCATTTTGA 393
Qy      81  AsnMetAsnLeuArgThrIleuSerGlyValAlaArgAspMetIleuGly----- 97
Db      394  AACATGAACCTGCGCAACCTCTCGAGAGAGCAGCGGATGACATGAAAGCAATTCACCA 453
Qy      97  ----- 97

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Db 454 GAAGATCTGAAGCAGATGACTGACCAAGGACCAAGCAAGAAAAATGCCAGGAATT 513  
Qy 98 -----11eser 99  
Db 514 TCACAGCTGTGCACAAAGATAGTGTCCACAGCTGCAGAGACAAAGAAACAGAGAAATTTC 573  
Qy 100 G1AA1aMetGluGluGluGluValAlaThrAla1aGluThrGluGluGluGlu11eserGln 119  
Db 574 CAACCTATGGAACAAAGAAAGGTGTCCACAGCACAAGACAGAAAGAAACAAAGAAATTTCA 633  
Qy 120 A1aMetGluGluGluGluValAlaThrAla1aGluThrGluGluGluGluGlu11eserGln 139  
Db 634 GCTATGGAACAAAGAAAGGTGTCCACAGCACAAGACAGAAAGAAACAAAGAAATTTCA 693  
Qy 140 ThrTrpAspTyrTyrSerSerHisValMetThrTyrPheAlaGluGluGluGluAspValArgArg 159  
Db 694 ACATGGGACTACAGAGAGTCAAGTATGACCAAAATTCGCTGAGAGAGAGAGTACGTCGT 753  
Qy 160 SerPheGluAsnThrAla1aAspTrpProGluMetGluThrLeuAlaGluValAlaPheAsp 179  
Db 754 AGTTTGAACAAACACTGCTGACTGACCGGAAATGCAACGTTGGCTGCTTTGAT 813  
Qy 180 SerAspArgTrpGluPheArgProArgThrValAlaLeuHisGluTyrSerGluTyrLeuGly 199  
Db 814 TCAGACCGGTGGGCTTCGGCTTCGACGGGTGTTCGACGGAAAGTCAAGAAATTTGG 873  
Qy 200 LysSerAlaLeuAlaArgArgGluLeuGluCysTrpAlaGluGluGluTyrGluTyrGlnGly 219  
Db 874 AAATCGGCTTACGACAGAGAGATCGTGTGTGTGGGCGCAAGGTGACCTTACCAAGGA 933  
Qy 220 MetPheSerTyrValPhePheLeuProValArgGluMetGluArgTyrLysGluSerSer 239  
Db 934 ATGTTCTCTCAGCTTCTTCTCCCTAGAGAGATGACGGGAAAGAAAGAGAGAGCT 993  
Qy 240 ValThrGluPheLeuLeuSerArgGluThrProAspSerGlnAlaProValThrGluLeuMet 259  
Db 994 GTCCAGAGTTCATCTCCAGAGAGTGCAGAGCTCCAGGCTCCGGTACAGAGATCTATG 1053  
Qy 260 SerArgProGluArgTyrLeuPheLeu1e11aAspGluPheAspAspLeuGluSerValLeu 279  
Db 1054 TCCGACCAAGAAAGGCTGTGTTCATCATGACGTTTCATGACCTGGGCTGTGTCTC 1113  
Qy 280 AsnAsnAspThrTyrLeuCysLysAspTrpAlaGluTyrGlnProProPheThrLeu1e 299  
Db 1114 AACATGACACAAAGCTGTGCAGAAAGCTGGCTGAGAGAGAGCTCCCTTACCTCAT 1173  
Qy 300 ArgSerLeuLeuArgTyrValLeuLeuProGluSerPheLeu1eValThrValArgAsp 319  
Db 1174 CGCAGTCTGTGAGAGAGTCTGTCTCTGAGTCTTCTGATCTGACCGTCAAGAGAC 1233  
Qy 320 ValGluThrGluLysLeuLysSerGluValAlaSerProArgTyrLeuLeuValArgGlu 339  
Db 1234 GTGGGACAGAGAACTCAAGTCAAGAGTCTGTCTCCCTTACCTGTATGAGAGAG 1293  
Qy 340 11eserGluGluGluGluGlu1e11aLeuLeuLeuGluArgGluTyrLeuGluHisGlnLys 359  
Db 1294 ATCTCCGGGAAACAAAGATCACTTGTCTTGAAGCGGAGATGGAGACATCAGAGAG 1353  
Qy 360 ThrGluGluLeuArgAla11eMetAsnAsnArgGluLeuLeuAspGluCysGluValPro 379  
Db 1354 ACACAAAGGTTGCGTGCATATCAACAAACGTGAGCTGCACCACTGACAGGTGCC 1413  
Qy 380 AlaValGluSerLeu1eCysValAlaLeuGluLeuGluAspValAlaGluGluSerVal 399  
Db 1414 GCCGTGGGCTTCTCATCTGCGTGGCTTCGACGCTGCAGAGACGTGTGTGGGAGAGGCTC 1473  
Qy 400 AlaProPheAsnGluThrLeuThrGluLeuHisAlaAlaPheValPheHisGluLeuThr 419  
Db 1474 GCCCCTTCAACCAAGCTCAAGGCTGCAGCGCTTTTGGGCTTTCATCAGGTCAAC 1533  
Qy 420 ProArgGluValValArgArgCysLeuAsnLeuGluGluArgValValLeuLysArgPhe 439

Db 1534 CTTGAGAGCGTGTCCGCGCTGTCTCATCTGAGAGAGAAAGTGTCTGAGAGCGCTTC 1593  
Qy 440 CysArgMetAlaValGluGluValTyrAsnArgLysSerValPheAspGluAspAspLeu 459  
Db 1594 TGCCGTATGCTGTGAGAGAGTGTGAATAGAAATGACAGTGTGTGATGAGACACTTC 1653  
Qy 460 MetValGluGluGluGluGluSerGluLeuArgAlaLeuPheHisMetAsn11eLeuLeu 479  
Db 1654 ATGGTTCAAGGACCTGGGAGGTGTGACCTCGTCTGTTCACATGAACATCTTCTTC 1713  
Qy 480 ProAspSerHisCysGluGluTyrTyrThrPhePheHisLeuSerLeuGluAspPheCys 499  
Db 1714 CCAGACAGCCACTGTGAGAGTACTACACTTCTTCCACTCTGACTCCAGAGACTTCTGT 1773  
Qy 500 AlaAlaLeuTyrTyrValLeuGluGluLeuGluGluGluProAlaLeuCysProLeuTyr 519  
Db 1774 GCCGCTTGTATCAGTGTATGAGAGGCTGGAAATTCAGACCAAGCTCTGCGCTGTATC 1833  
Qy 520 ValGluTyrThrTyrValArgSerMetGluLeuLysGlnAlaGluPheHisGluHisSerLeu 539  
Db 1834 GTTAGAAGACCAAGAGGTCCATGAGCTTAAACAGCAGAGCTTCCATATCCACTGCTT 1893  
Qy 540 TrpMetLysArgPheLeuPheGluLeuValSerGluAspValArgAspProLeuGluVal 559  
Db 1894 TGGATGAAGCTTCTTCTTGTGCTGTGAGCGAAGACGTAGAGAGGCCACTGAGAGTC 1953  
Qy 560 LeuLeuGluCysProValProLeuGluValLysGluLysLeuLeuHisTyrValSerLeu 579  
Db 1954 CTGCTGGGCTGTCTCCGTTCCCTGGGGGTGAAGAGCAAGCTTGTGACTGGGTCTCTCTG 2013  
Qy 580 LeuGluGluGlnProAsnAlaThrThrProGluAspThrLeuAspAlaPheHisCysLeu 599  
Db 2014 TTGGGTGACGACCTTAATGACCAACCCAGAGAACCCCTGACGCTTCCACTGCTT 2073  
Qy 600 PheGluThrGluAspLysGluPheValArgLeuAlaLeuAsnSerPheGluGluValTyr 619  
Db 2074 TTCAGACTCAAGCAAGAGATTGTTCCTGCTGACATTAACCTTCCAGAGAGTGTGG 2133  
Qy 620 LeuPro11eAsnGluAsnLeuAspLeu1eAlaSerSerPheCysLeuGlnHisCysPro 639  
Db 2134 CTTCGATTAACCAAGACCTGAGCTTGATGACATCTTCTGCTCCAGACACTGTCCG 2193  
Qy 640 TyrLeuArgLys11eArgValAspValLysGlu11ePheProArgAspGluSerAlaGlu 659  
Db 2194 TATTTGGGAAATTCGGGTGATGTCAAGGGATCTTCCMAAGATGAGTCCGCTGAG 2253  
Qy 660 AlaCysProValValProLeuTrpMetArgAspThrLeu11eGluGluGlnTyrGlu 679  
Db 2254 GCATGTCTGTGTCCCTCTATGAGATCGGAGTAAACCTCTCATTTGAGAGAGTGGGA 2313  
Qy 680 AspPheCysSerMetLeuGluTyrHisProHisLeuArgGluLeuAspLeuGluSerSer 699  
Db 2314 GATTTCTGTCCATGCTTTGGACCCACCACTGGCGGAGCTGGGAGCAGC 2373  
Qy 700 11eLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCysLys 719  
Db 2374 ATCTGACAGAGCGGGCATGAGACCTGTGTGCCAAGCTGAGAGATCCCACTGAGAG 2433  
Qy 720 11eGluThrLeuMetPheArgAsnAlaGlu11eThrProGluValGlnHisLeuTrpArg 739  
Db 2434 ATACAGACCTCGATGTTTGAATATGACAGATTTACCTCGGTGTGTGCACACTTGGAGA 2493  
Qy 740 11eValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGluGluTyrHisLeuLysGlu 759  
Db 2494 ATCGTCAATGGCAACCGTAACCTTAAGATCCCTCAACTTTGGAGGACCACTGAGAGAA 2553  
Qy 760 GluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSerLeu 779  
Db 2554 GAGGATGTAAGATGGGTGGAAGCTTAAACCAACCAAAATGTTGTTGAGTCTTTG 2613  
Qy 780 ArgLeuAspCysCysGluLeuThrHisAlaCysThrLeuLys11eSerGln11eLeuThr 799  
Db 2614 AGGCTGAGTGTGTGATGAGCCCATGCTGTTAACCTGAAGATCTCCAAATCTTACG 2673

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QY 800 ThisSerProSerLeuLYSerLeuSerLeuAlaGlyAseuLYValThrAspGlnGlyVal
Db 2674 ACCTCCCCACGCTGAATCTCTGAGCTGGAGAGAAACAAGTACACAGACGAGAGTA 2733
QY 820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLYLeuGln 839
Db 2734 ACGCTCTCAGTGAAGCTTGGGGGTCTCCCGAGTCCGCTGCAAGACTGATCTGAGG 2793
QY 840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db 2794 GACTGTGCATCAGACGCAACGGGTGGCCAGAGTCTGGGCTCAAGCCCTGTGACAGACGG 2853
QY 860 SerLeuThrAlaLeuCysLeuSerAsnAsnSerLeuGlyAseuGlnGlyValAsnLeuLeu 879
Db 2854 AGCTTGACACACCTGTGCTTATCCAAACAAGCCTGGGGAAGAGATGAATTAATCTACTG 2913
QY 880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db 2914 TGTGCATCAGTGAAGCTTCCCACTGTAGTCTGCAGAGGCTGATCTGAATCAGTGCAC 2973
QY 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAseuSerThrLeuThr 919
Db 2974 CTGACACAGGCTGGCTGTGTTCTTCTTCACTTGGCTTAAGGTAATGCTCAATGGCTGACG 3033
QY 920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLYLeuLeuCysGlyVal 939
Db 3034 CACTGAGCTTGAATGAACCTCTGTGAAGACATGGCGTGAAGCTTCTGTGCAAGTTC 3093
QY 940 MetArgGluProSerCysHisLeuGlnAspLeuGlnValLYCysHisLeuThrAla 959
Db 3094 ATGAGAGAACCATCTTGTCAATCTCCAGGACCTGAGGTTGTAAGTGCATCTCACCCGC 3153
QY 960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLYSerLeuAsp 979
Db 3154 GCGGTCTGTGAAGCTGTCTCTGTGTATCTCGAGAGACAGACACTTGAAGAGCTGTGAT 3213
QY 980 LeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlyLYLeuLYGln 999
Db 3214 CTCACGACAAATGCCCTGGGTGAACGTTGGGTGCTGCGCTGTGAGAGACTGAAACAA 3273
QY 1000 LYAsnSerValLeuThrArgLeuGlyLeuLYAsnLYCysGlyLeuThrSerAspCys 1019
Db 3274 AAGAACAAGTGTTCGACGAGACTGGGTTGAAGGATGTGACTGACTTGTGATTGCTGT 3333
QY 1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLYGln 1039
Db 3334 GAGGCACTCTCTTGGCCCTTCTCGCAACCGGCATCTGACCAAGTCTAAACCTGGTGCAG 3393
QY 1040 AsnAsnProSerProLYGlyMetMetLYLeuCysSerAlaPheAlaCysProThrSer 1059
Db 3394 AATAACTTCAGTCCCAAGAAATGATGAAGCTGTGTGGCCCTTGGCTGTGCCACGCT 3453
QY 1060 AsnLeuGlnIleLeuGlyLeuThrLYSerGlnTYrProValGlnIleArgLYLeuLeu 1079
Db 3454 AACTTACGATTAATTGGGCTGTGAAATGCGCATGCTGTGCAATTAAGAAAGTGTCTG 3513
QY 1080 GluGluValGlnLeuLeuLYProArgValIleAspGlySerThrHisSerPheAsp 1099
Db 3514 GAGGAGAGGCACTCAACACCCGAGTCTGAATTAAGGTAAGTGTGCAATCTTTGAT 3573
QY 1100 GluAspAspArgHis 1104
Db 3574 GAAAGTACCGGTAC 3588

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RESULT 7
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication NO. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services

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; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
US-10-677-943-23
Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 5741.50 Matches: 1098
Percent Similarity: 96.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
Gaps: 1
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QY 1 MetGluGlyAspLYSerLeuThrPheSerSerTYrGlyLeuGlnTYrCysLeuTYrGlu 20
Db 154 ATGAGAGAGACAAATCGCTCACTTTCAGCTACGCGCTGCATGTGTCTCATAG 213
QY 21 LeuAspLYGluGluPheGlnThrPheLYGluLeuLYLysLYSerSerGlySer 40
Db 214 CTAGACAGAGAAATTTACACATTCAGAAATTAATCTAAAGAAATCTTCAGAAATCG 273
QY 41 ThrThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
Db 274 ACCACATCTCTATTTCCACATTTGAATGCAAGATGCAACGTGAATGTCTGGCACTC 333
QY 61 LeuLeuHisGluTYrTYrGlyAlaSerLeuAlaThrAspIleSerIlePheGlu 80
Db 334 CTCTTGATGATGATTAATGAGCATGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 393
QY 81 AsnMetAsnLeuArgTYrThrLeuSerGluLYAsnLYAspAspMetLYLeu----- 97
Db 394 AACATGAACCTGCAACCTCTCGAGAGAGGACGGGATGACATGAAGAAACATTACCA 453
QY 97 ----- 97
Db 454 GAAATCTCTGAAGACAGATGATGACCAAGACCAAGCAAGAAAGTCCAGGAATT 513
QY 98 -----IleSer 99
Db 514 TCACAAGCTGTGCAACAAGATAGTGCACAGCTGCAGACAAAGAAAGCAAGAAATTCA 573
QY 100 GlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnIleSerGln 119
Db 574 CAAGCTATGAAACAAGAGGTGCAACGACAGACAGACAGAAAGAAACAAGAAATTTCA 633
QY 120 AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnIleGlyLYAsp 139
Db 634 GCTATGAAACAAGAGGTGCAACGACAGACAGACAGAAAGAAACAAGACATGAGGTAC 693
QY 140 ThrTYrAspTYrLYSerHisValMetThrLYPheAlaGluGluGluAspValArgArg 159
Db 694 ACATGGGACTCAAGAGTCAAGTATGATGACCAATTCCTGCTGAGGAGATGATGCTGT 753

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QY 160 SerPheGluAenThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyValaPheAsp 179  
Db AGTTTTGAAAACACTGCTGCTGACGGCCGGAATGCAACGTTGGCGTGCTTTTAT 813  
QY 180 SerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSerGlyTleGly 199  
Db TCAGACCGGTGGGGCTTCGGCTCGCACGGGTGGTTCTGCACGAAAGTCAGAAATTGGG 873  
QY 200 LysSerAlaLeuAlaArgArgTleValLeuCystrTrpAlaGlnGlyGlyLeuTrGlnGly 219  
Db AAATCGGCTTAGCCAGAAAGATCGTGTGCTGGCGGCAAGGTGACCTTACACAGGA 933  
QY 220 MetPheSerTrpValPhePheLeuProValaArgGluMetGlnaGlyLysGlyLysSer 239  
Db ATGTTCTCTCAAGCTTCTTCTCCCGCTAGAGATGACGGCAAGAGAAAGAGACGT 993  
QY 240 ValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet 259  
Db GTCAAGATTCATCTCCAGGAGTGGCCAGACTCCAGGCTCCGGTACCGAAGTCAAG 1053  
QY 260 SerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu 279  
Db TCCCGACCAAGAAAGCTGTGTTCATCATGACGGTTTCATGACCTGGGCTGTCTTC 1113  
QY 280 AsnAsnAspThrLysLeuCyLeuAspTrpAlaGlyLysGlnProPheThrLeuIle 299  
Db AACCATGACACAAAGCTCTGCAGAAAGCTGGCTGGAAGACCTCCCTTCACCTTCATA 1173  
QY 300 ArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeuIleValThrValaArgAsp 319  
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QY 320 ValGlyThrGluLysLeuLysSerGlyValaIleSerProArgTrpLeuLeuValaArgGly 339  
Db GTGGGACAGAGAAAGCTCAAGTCAAGAGTCCGTGTCTCCCGTTACCTTTAGTTAAGGA 1293  
QY 340 IleSerGlyGlnGlnArgIleHisIleLeuLeuGluLysArgGlyIleGlyLysHisGlnLys 359  
Db ATCTCCGGGGAAACAAAGATCACTTGTCTGTGACCGGGAAATGGTGAACATCAGAAAG 1353  
QY 360 ThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValaPro 379  
Db ACAAAGGGTGTGGCGATCATCAACAACGTTGAGCTGTGCACATGTGCAGGTGCGCC 1413  
QY 380 AlaValGlySerLeuIleCysValaIleLeuGlnLeuGlnAspValaIleGlyLysSerVal 399  
Db GCCGTGGGCTCTCATGTGGGTGGCCCTGCAGCTGCAGAGACGTGGTGGGGAAGAGCTC 1473  
QY 400 AlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr 419  
Db GCCCCCTTCAACCAACGCTCAAGGCTGCACGCGCTTTTGGCGTTTCATCAGCTCACCC 1533  
QY 420 ProArgGlyValaValaArgArgCysLeuAsnLeuGlnGluArgValaValLeuLysArgPhe 439  
Db CCTGAGGCGGTGTCGGCGCTGTCTCAATCTGAGGAAAGAGTTGTCTTAAGCGCTTC 1593  
QY 440 CysArgMetAlaValaGlnGlyValaTrpAsnArgLysSerValaPheAspGlyAspAspLeu 459  
Db TGCCTATGCGTGTGAGAGAGTGTGGAATAGAAAGTCAAGTCTTTGATGAGAGAGCTTC 1653  
QY 460 MetValGlnGlyLeuGlyGlySerGlyLeuLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479  
Db ATGGTTCAAGAGACTGGGAGAGTGTGAGCTCCGTGTCTGTTCACATGAACATCTTCTTC 1713  
QY 480 ProAspSerHisCysGlnGluTrpTrpThrPhePheHisIleuSerLeuGlnAspPheCys 499  
Db CCAAGACACCACTGAGAGAGTACTACACTTCTTCCACCTCAAGTCTCAAGACTCTGTCT 1773  
QY 500 AlaAlaLeuLeuTrpValaLeuGlnGlyLeuGlnIleGlnProAlaLeuCysProLeuTrp 519  
Db GCCCGCTTGTACTAGTGTTAAGAGGCTTGGAAATCGAGCCAGCTCTGCGCTGTGAC 1833  
QY 520 ValGluLysThrLysArgSerMetCysLeuLeuGlnAlaGlyPheHisIleHisSerLeu 539

Db 1834 GTTGAAGACCAAGAGGCTCCATGAGCTTAAACAGGAGGCTTCAATATCACTTCCCTT 1893  
QY 540 TrpMetLysArgPheLeuPheGlyLeuValaSerGlyAspValaArgArgProLeuGluVala 559  
Db TGGATGAAGGCTTCTTCTTTGGCTCTGTGAGCGAACAAGTAAGAGAGCCACTGAGAGTC 1953  
QY 560 LeuLeuGlyCysProValaProLeuGlyValaLysGlnLysLeuLeuHisIleTrpValaSerLeu 579  
Db CTGCTGGGCTGTCCCGTTCCTCGGGGTGAAGAGAGGCTTGTGCACTGGGTCTTCTCG 2013  
QY 580 LeuGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeu 599  
Db TTGGGTCAAGCCTTAATGCCACCAACCAAGAGACCTTCGAGCGCTTCCACTGTCTT 2073  
QY 600 PheGluThrGlnAspLysGlnPheValaArgLeuAlaLeuAsnSerPheGlnGluValaTrp 619  
Db TTCCAGACTCAAGACCAAGAGTGTTCCTGCTGCACTTAAACGCTTCCAAAGAGTGTGG 2133  
QY 620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639  
Db CTTCGATTAACCAAGACTGGAAGCTTATGATGATCTTCTTGTGCTCCAGCACTGTCCG 2193  
QY 640 TyrLeuArgLysIleArgValaAspValaLysGlyTlePheProArgAspGlyLysSerAlaGlu 659  
Db TATTTGGGAAATTCGGGTGATGTCAAAGGATCTTCCCAAGATGAGTCCGCTGAG 2253  
QY 660 AlaCysProValaIleProLeuTrpMetArgAspLysThrLeuIleGlnGlnGlnTrpGlu 679  
Db GCAATGCTGTGTGCTCTCTATGATTCGGGATGAAGACCTCATTTAGAGAGCACTGGGAA 2313  
QY 680 AspPheCysSerMetLeuGlyThrHisProHisIleuArgGlnLeuAspLeuGlySerSer 699  
Db GATTTCTGTTCACAGCTTGGCACCCACCACTGGCGGAGCTGAGCAGCAGCAGC 2373  
QY 700 IleLeuThrGlnaArgAlaMetLysThrLeuCyAlaLysLeuArgHisIleProThrCysLys 719  
Db ATCTGACAGAGCGGCGCATGAAGACCTGTGTGCAAGCTGAGAGCTCCACCTGTGAG 2433  
QY 720 IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValaGlnHisIleLeuTrpArg 739  
Db ATACAGACCTCTGATGTTTAAGAAATGACACAGATTAACCTCTGTGTGCAACCTCTGAGA 2493  
QY 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisIleuLysGln 759  
Db ATCGTCAATGGCAACCGTAACCTTAAGATCCCTCACTTGGAGGACCAACCTTAAGAA 2553  
QY 760 GluAspValaArgMetAlaCysGlnAlaLeuLysHisIleProLysCysLeuLeuGlySerLeu 779  
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QY 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTrpTrpLysIleSerGlnIleLeuThr 799  
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QY 800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValaThrAspGlnGlyVala 819  
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QY 840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValaSerAspArg 859  
Db GACTGTGACATCAAGCCACAGGGTTGCCAAGTGTGACCTTCAGCTTCAGCAACCGG 2853  
QY 860 SerLeuThrHisLeuCyLeuSerAsnAsnSerLeuGlyValaGlnGlyValaAsnLeuLeu 879  
Db AGCTTGACACACCGTGTCTATCCAAACAAGCCTGGGGAACGAAGGTGTAATCTACTG 2913  
QY 880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899

Db 2914 TGTGATCATGAGGCTTCCCACTGATGTCGACAGAGCTGATCTGATCATGTCAC 2973  
Qy LeuApThrAlaGlyCyseGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThr 919  
Db 2974 CTGACACGCGCTGGCTGGTCTCTTGCACTTGCGCTTAATGGAATCTCATGCTGACG 3033  
Qy HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIleLeuLeuCyseGluVal 939  
Db 3034 CACGACGACCTTAGCATGACCTCTGGAGAAGCAATGGGTGAACCTTCTGCGCAGGTC 3093  
Qy 940 MetArgGluProSerCyseHisLeuGlnAspLeuGluLeuValIleCyseHisLeuThrAla 959  
Db 3094 ATGAGAGAACCATCTTGTCATCTCCAGACCTCGAGTTGGTAAAGTCATCTCACTCC 3153  
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Db 3154 GCGGCTGTGAGAGCTGTCTGCTGTGATCTCGAGAGACGACACCTGAAGAGCTGAGT 3213  
Qy 980 LeuThrAspAsnAlaLeuGlyAspGlyValIleAlaLeuCyseGluGlyLeuLeuSerGln 999  
Db 3214 CTCACGACCATGCGCTGGGTGACGCTGGGTGCTGCGCTGTGCGAGGACGTGAAGCA 3273  
Qy 1000 LysAsnSerValLeuThrArgLeuGlyLeuValIleCyseGlyLeuThrSerAspCyse 1019  
Db 3274 AAGAACAGTGTCTGACGAGACTCGGCTTGAAGCATGTGACCTGATTTGCTGT 3333  
Qy 1020 GluAlaLeuSerLeuAlaLeuSerCyseAsnArgHisLeuThrSerLeuAsnLeuValGln 1039  
Db 3334 GAGGACCTCTCTGCTGCTCTCTCTGCAACCGGCACTGACGACGCTGAACCTGTGACG 3393  
Qy 1040 AsnAsnPheSerProLysGlyMetMetLysLeuCyseSerAlaPheAlaCyseProThrSer 1059  
Db 3394 AATACTTCAGTCCCAAGAAATGATGAACTGTGTGGCTTTGCTGCTGCCACGCTCT 3453  
Qy 1060 AsnLeuGlnIleIleGlyLeuThrTrpLysTrpGlnTrpProValGlnIleArgLysLeuLeu 1079  
Db 3454 AACTTACGATTAATGGGCTGTGGAATGGCAGTACCTGTGCAATGAAGAAGCTGCTG 3513  
Qy 1080 GluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAsp 1099  
Db 3514 GAGGAAGGCGACTAAGTCAAGCCCGAGTGTGAATGACGATGTCATTTCTTTGAT 3573  
Qy 1100 GluAspAspArgHis 1104  
Db 3574 GAAGATGACCGGTAC 3588

RESULT 8  
US-10-216-645-3  
; Sequence 3, Application US/10216645  
; Publication No. US20030125282A1  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, BERTRAM  
; APPLICANT: LESSL, MONIKA  
; APPLICANT: PETERS-KOTTIG, MICHAEL  
; APPLICANT: BECKMANN, GEORG  
; TITLE OF INVENTION: HUMAN MATER PROTEINS  
; FILE REFERENCE: SCH-1910  
; CURRENT APPLICATION NUMBER: US/10/216, 645  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3830  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-216-645-3

Alignment Scores:  
Pred. No.: 0 Length: 3830  
Score: 5683.50 Matches: 1087  
Percent Similarity: 95.87% Conservative: 5

Best Local Similarity: 95.43% Mismatches: 12  
Query Match: 80.34% Indels: 35  
DB: 15 Gaps: 2  
US-10-066-521-6 (1-1344) x US-10-216-645-3 (1-3830)

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Db 1 ATGGAAGAGAACAAATGCTCACCTTTTCCAGCTACGGGCTGCAATGGGTCTCATGAG 60  
Qy 21 LeuAspLysGluGluPheGlnThrPheLysGlyLeuLeuLysLysSerSerGluSer 40  
Db 61 CTAGCAAGAGAAATTTCAACATTTCAAGAAATTTAAAGAAATTTCTCAAAATCG 120  
Qy 41 ThrThrCyseSerIleProGlnPheGluIleGluAsnAlaAsnValGluCyseLeuAlaLeu 60  
Db 121 ACCAATCTCTAATTCACAGTTGAATTCAGAAATGCAACGTGAAATGTCGACCTC 180  
Qy 61 LeuLeuHisGluTrpTrpGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80  
Db 181 CTCTTGATGATGATTAATGAGACATCGCTGGCTGGCTAGTCAATGATTCATTTGAA 240  
Qy 81 AsnMetAsnLeuArgThrLeuSerGlyLysAlaArgAspAspMetLysLysSerGln 100  
Db 241 AACATGAACCTGCCAACCTCTCGGAGAAAGGACCGGATGACATGAAATAATTCACCA 300  
Qy 101 -----AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGln--- 115  
Db 301 GATCTGAAGACACGATGATGACCAAGACCAAGCAAGAAAGATGCCAGAAATGAA 360  
Qy 115 ----- 115  
Db 361 TATGACATGACTAAGCTTATCTTGGGGGTGTCTGACATCTGACTCGAATTAATAAC 420  
Qy 116 -----GluIleSerGlnAlaMetGluGlnGly 125  
Db 421 AAGTATGTGAATTCATTTCTTTTTCGCAAAATTTCAAGCTAATGAACAAGAAAGT 480  
Qy 126 AlaThrAlaAlaGluThrGluGlnGlnGlyHisGlyGlyAspThrTrpAspTrpLysSer 145  
Db 481 GCCACAGACAGACAGACAGAAACAGAGATGAGGTGACACATGGGACTTACAAAGT 540  
Qy 146 HisValMetThrLysPheAlaGluGluGluAspValArgArgSerPheGlyAsnThrAla 165  
Db 541 CACGTGATGACCAATTCGCTGAGAGAGAGATGTACGTGATTTGAAAACTCTCT 600  
Qy 166 AlaAspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPhe 185  
Db 601 GCTGACTGGCCGGAATGCAAAAGTGGCTGTGTTGATTCAGACCGGTGGGCTTC 660  
Qy 186 ArgProArgThrValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 205  
Db 661 CGGCTCGCAGGGTGTCTTCACGGAAGTCAGAAATGGGAATCGCTCTAGCCGA 720  
Qy 206 ArgIleValLeuCyseTrpAlaGlnGlyLeuTrpGlnGlyMetPheSerTrpValPhe 225  
Db 721 AGAATCGTGTGTGTGGCCGCAAGGTGACTTACAGGGAATGTCTCTACGCTTC 780  
Qy 226 PheLeuProValArgGluMetGlnArgLysLysGluSerSerValThrGluPheIleSer 245  
Db 781 TTCCTCCCGTTAAGAGATGACAGGAAGAAAGAGACATGTTCACAGATTCATCTCC 840  
Qy 246 ArgGluTrpProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeu 265  
Db 841 AGGAGTGGCCAGACTCCAGAGCTCCGCTGACGAGATCAAGTCCCGACGAAAGGCTG 900  
Qy 266 LeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeu 285  
Db 901 TTGTTCAATTAAGAGGTTTGATGACCTGGGCTGTGCTCTCAACAAATGAACAAGCTC 960  
Qy 286 CyseLysAspTrpAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgLys 305  
Db 961 TGCAAAAGCTGGGCTGAAGACACCTCTCGTTACCTCATACCGCATGCTGTGAGGAG 1020

QY 306 ValLeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeu 325  
Db 1021 GTCCGCTCCCTGAGTCTTCTGATCGTCACCGTCAGAGAGCGGGACAGAGAGCTC 1080  
QY 326 LysSerGluValIleSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArg 345  
Db 1081 AAGTCAGAGGTCGTGTCCCGCTTACCTGTAGTAGAGAACTCCGGGGAAACAAAGA 1140  
QY 346 IleHisLeuLeuGluArgGlyIleGlyGlnHisGlnLysThrGlnGlyLeuArgAla 365  
Db 1141 ATCCACTTGCTCTTGAAGCGGGAGTTGTGTAGCATCAGAAAGACAAAGAGTTGCTGCG 1200  
QY 366 IleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIle 385  
Db 1201 ATCATGAACAACCGGAGCTCTCGACAGTGCAGCGTCCGCGGTGGGCTCTCTCATC 1260  
QY 386 CysValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThr 405  
Db 1261 TGCCTGGCCCTGCAGCTGCAGAGACGTGGTGGAGAGACGTGCGCCCTTCAACCAACG 1320  
QY 406 LeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArg 425  
Db 1321 CTCACAGGCTTGCAAGCCGCTTTGTGTGTTCATCAGCTCACCCCTCAGAGGCTGTCGG 1380  
QY 426 ArgCysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGlu 445  
Db 1381 CGCTGTCTCAATCTGAGGAAGAAGTTGCTCTGAAGCGCTTCTGCGTATGGCTGTGAG 1440  
QY 446 GlyValITrPasnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGly 465  
Db 1441 GGAGTGTGAATAGAGAACTGAGTGTTCACGTGACGATCCATAGTTCMAAGACTCGGG 1500  
QY 466 GluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGlu 485  
Db 1501 GAGTGTGAGCTCCGTGCTCTGTTTCATGACATGACATCTTCTCCAGAGCCACTGTAG 1560  
QY 486 GluTyrTyrThrPhePheHisAlaSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505  
Db 1561 GAGTACTACACTTCTTCCACTGACTGCTCCAGAGCTTCTGAGCGCTTGATAGACTG 1620  
QY 506 LeuGluGlyLeuGluIleGluProAlaLeuCysProLeuTyrValGluLysThrLysArg 525  
Db 1621 TTAGAGGCTGTGAATGAGACAGCTCTGCTGCTGTGACGTGAAACAAAGAGG 1680  
QY 526 SerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTyrMetLysArgPheLeu 545  
Db 1681 TCCATGAGCTTAAACAGGCAAGCTTCCATTCACCTGCTTGGATGAAAGCTTTCTTG 1740  
QY 546 PheGlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProVal 565  
Db 1741 TTTGGCCCTGTGAGAGAAAGATGTAAGAGGCACTGAGGTCCTGGGCTGTCCGCTT 1800  
QY 566 ProLeuGlyValLysGlnLysLeuLeuHisTyrPValSerLeuLeuGlyGlnGlnProAsn 585  
Db 1801 CCCCTGGGGGTGAAGCAAGACTTCTGCACTGGGTCTCTGTGGGTCAACAGCTATAT 1860  
QY 586 AlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGlnThrGlnAspLys 605  
Db 1861 GCCACACCCCAAGAGACACCTGAGAGCTTCCACTGTCTTTCGAACTCAAGACAA 1920  
QY 606 GluPheValArgLeuAlaLeuAsnSerPheGlnGluValTyrPLeuProIleAsnGlnAsn 625  
Db 1921 GAGTTTGTTCGCTTGCACTTAAACAGCTTCCAGAAAGTGGCTTCCGATTAACAGAAC 1980  
QY 626 LeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArg 645  
Db 1981 CTGGACTTGATAGCATCTTCTTCTGCTCCAGCACTGTCCGATATTTCGGAAAAATTGG 2040  
QY 646 ValAspValLysGlyIlePheProArgAspGluSerAlaGluAlaCysProValValPro 665  
Db 2041 GTGATGTCAAAAGGATCTTCCCAAGAGATGATGTCGCTGAGGCAATGTCGTGTCTCCT 2100

QY 666 LeuITrMetArgAspLysThrLeuIleGluGluGlnITrPValAspPheCysSerMetLeu 685  
Db 2101 CTATGATGGGGATTAAGACCTCATTTGAGAGAGAGTGGAGATTTCTCTCATCTT 2160  
QY 686 GlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAla 705  
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QY 726 ArgAsnAlaGlnIleThrProGlyValGlnHisLeuITrPArgIleValMetAlaAsnArg 745  
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QY 766 CysGluAlaLeuLysHisProLysCysAlaLeuGluSerLeuArgLeuAspCysCysGly 785  
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QY 846 ThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCys 865  
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QY 866 LeuSerAsnAsnSerLeuGluLysGlnGlyValAlaAsnLeuCysArgSerMetArgLeu 885  
Db 2701 CTATCCAACAACGCTGGGGAACGAAAGGTAAATCTACGTGTCAATCATAGAGCTT 2760  
QY 886 ProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisAlaLeuAspThrAlaGlyCys 905  
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QY 906 GlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTyrLeuThrHisAlaSerLeuSerMet 925  
Db 2821 GATTTCCTTGCACTTGCGCTTATGGTAACTCATGTGCTGACGCACTGAGGCTTATGATG 2880  
QY 926 AspProValGluAspAsnGlyValLysLeuLeuCysGlnValMetArgGluProSerCys 945  
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QY 946 HisLeuGlnAspLeuGluLeuValLysCysHisAlaLeuThrHisAlaCysCysGluSerLeu 965  
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QY 986 GlyAspGlyGlyValAlaAlaAlaLeuCysGluGlyLysLeuGlnLysAsnSerValLeuThr 1005  
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QY 1006 ArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGlnAlaLeuSerLeuAla 1025  
Db 3121 AGACTCGGTTGAAGGCAATGTGACTGATCTTGTATGCTGTGAGGCACTCTCTTGACC 3180  
QY 1026 LeuSerCysAsnArgHisAlaLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLys 1045



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Db      3181 CTTTCCTGCAACCGGCACTCTAACCGATTAACCTGGTGCAGATTAACCTTACGATCCCAA 3240
QY      1046 GlywectivlyLeuCYseSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGly 1065
Db      3241 GGAATGATGAAGCTGTGTGTCGCCCTTTCCTGTCCACAGCTTAACCTTAACATATATGGG 3300
QY      1066 LeuTrpLyseTrpGlnTrpProValGlnIleArglyLeuLeuGluGluValGlnLeuLeu 1085
Db      3301 CTGGGAAATATGGCAGTATCCCTGTGCAATATAGGAAGCTGTGGAGGAAGTGCACCTCTCTC 3360
QY      1086 LysProArgValAlaValIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
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RESULT 9
US-10-092-900A-347
Sequence 347, Application US/10092900A
Publication No. US20040043382A1
GENERAL INFORMATION:
APPLICANT: Padigar, Muralidhara
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Taudier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Li, Li
APPLICANT: Zernhusen, Bryan D.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
APPLICANT: Gorman, Linda
APPLICANT: Miller, Charles E.
APPLICANT: Kekuda, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gangoli, Bsha A.
APPLICANT: Vernet, Corine A.M.
APPLICANT: Guo, Xiaojia Saaba
APPLICANT: Tchernev, Velizar T.
APPLICANT: Fernandes, Elma R.
APPLICANT: Caeman, Stacie J.
APPLICANT: Malyanhar, Uriel M.
APPLICANT: Gerlach, Valerie
APPLICANT: Liu, Yi
APPLICANT: Anderson, David W.
APPLICANT: Spaderna, Steven K.
APPLICANT: Carterton, Elina
APPLICANT: Lette, Mario W.
APPLICANT: Zhong, Haihong
APPLICANT: Alsobrook, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Bugees, Catherine B.
TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-290C
CURRENT APPLICATION NUMBER: US/10/092, 900A
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: USSN 60/274, 322
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/283, 675
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: USSN 60/338, 092
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: USSN 60/274, 281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/274, 191
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/325, 681
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: USSN 60/304, 354
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: USSN 60/279, 995
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: USSN 60/294, 899
PRIOR FILING DATE: 2001-05-31

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[illegible]

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Db 893 TGAACGCGGAGATGGTGAGCATCAGAAAGACAAAGGGTTGGTGCGATCAGAAACAACCG 952  
Qy 370 gGluLeuLeuAArgInCysGInValProAlaValGlySerleuHllecYsValAlaleuGI 390  
Db 953 TGACCTGCTTCAGCAAGTGCAGAGTGCCTGCGTGGCTCTCTCATCTGCAGTGGCCCTGCA 1012  
Qy 390 nLeuGIAnaPValValGIyGluSerValAlaProPheAnGIInThrLeuThrGIyleuHl 410  
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Qy 410 sAlaAlaPheValPheHlsgInLeuThrProAArgIylValValAArgAArgyleuAnle 430  
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Qy 450 gLySerValPheAArgPglYAAsPleuMetValGInGIyleuGIyGluSerGIyleuAr 470  
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Qy 510 uIlleGIuProAlaleuCysProleuTyrrValGIuLyethrLyAArgSerMetGIuleuLy 530  
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Qy 590 yAsPThrleuAAsPAlaPheHlscYsleuPheGIuThrGIAnaPlysgIuPheValArgle 610  
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QY 1070 nTy-ProValaIaIleArglyLeuLeuGluGluValaIleLeuLeuLysProArgVala 1090  
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RESULT 10  
US-10-399-443-5  
Sequence 5, Application US/10399443  
Publication No. US2004002869A1  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America, as Represented by the  
APPLICANT: Secretary, Department of Health & Human Services, The National Institute  
APPLICANT: Health  
APPLICANT: Nelson, Lawrence M.  
APPLICANT: Tong, Zhi-Bin  
APPLICANT: Nelson, Lawrence  
APPLICANT: Zhi-Bin, Tong  
TITLE OF INVENTION: Human Gene Critical to Fertility  
FILE REFERENCE: 4239-64785  
CURRENT APPLICATION NUMBER: US/10/399,443  
CURRENT FILING DATE: 2003-04-16  
PRIOR APPLICATION NUMBER: 60/241,510  
PRIOR FILING DATE: 2000-10-18  
PRIOR APPLICATION NUMBER: PCT/US01/10981  
PRIOR FILING DATE: 2001-04-04  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 3447  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-399-443-5

Alignment Scores:  
Pred. No.: 8.76e-276 Length: 3447  
Score: 2688.00 Matches: 554  
Percent Similarity: 66.49% Conservative: 186  
Best Local Similarity: 49.78% Mismatches: 293  
Query Match: 38.00% Indels: 81  
Gaps: 11

US-10-066-521-6 (1-1344) x US-10-399-443-5 (1-3447)

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QY 75 SerIleSerIlePheGluAsnMetAsnLeuArgThrIleuSerGluTyrgAlaArgAspArg 94  
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QY 95 MetLysLysIleSerGln----- 100  
Db 300 GTGAAACAGGGCTGAGAAAGAAATGACTTCTCCAGAAAAGACAGTAAATCAATCCAG 359  
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QY 136 HisGlyGlyAspThrTrpAspTyrgLysSerHisValMetThrLysPheAlaGluGlu 155  
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QY 156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175  
Db 504 GATCTACAC-----TATGACAGCCCAAGATGATAATTAATTTGCT 542  
QY 176 GlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrValIleHisGlyLys 195  
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Db 603 CAGAGAGTGGAGATGACGCTTTGGCCAGAGTATGCTTGGTGGGACAGGTTAA 662  
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Db 663 CTCTCCAAAATG---TCCTTGTCACTCTTCTGTTAGAAATAAGATGAC 719  
QY 236 LysGluSerSerValThrGluPheIleSerArgIuTrpProAspSerGlnAlaProVal 255  
Db 720 GAGAGAGACAGTTGGACAGCTGATGCTAAGAGAGTGTCCAGACTCTGGAGATCTAGT 779  
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Db 900 ATATACATCTGATGATGACAGCTCTGAGAAAGCTCTTCACTCACTCTTCTCAATC 959  
QY 315 ValThrValArgAspValGlyThrGluLysLeuLysSerGluValIleSerProArgTyrg 334  
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QY 335 LeuLeuValArgGlyLysSerGlyGluGlnArgIleHisLeuLeuLeuGluArgLysLys 354  
Db 1020 ATACTGGTGAAGAGCTGTGATGATCAAGAGATCTGATGATGATGATGATGATGATG 1079  
QY 355 GlyGluHisGluLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAsp 374  
Db 1080 AATGAGCTGATGAATAAATGATCTTCATCTCTGATGAATAAATGACAGCTGTTGAC 1139  
QY 375 GlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspVal 394  
Db 1140 CAATGCCAGGCCCTCTGTGTGCTCTCCCTGTGTGTAGAGTCTTACAGCTACAGAAAGAA 1199  
QY 395 ValGlyGluSerValAlaProPheAsnGlnThrPheThrGlyLeuHisAlaAlaPheVal 414  
Db 1200 CTGGGAAGAGATGACCTTACCTTCCAGAGCTTCAACCGGTTTGTATGCCAGTGGT 1259  
QY 415 PheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgVal 434  
Db 1260 TTTTACACAGCTCACTTGAAGAAAGCCCTTCCAGAGAGCCCTCACTCACTCAAGAAAGAA 1319  
QY 435 ValLeuLysArgPheCysArgMetAlaValGluGluValIleTrpAsnArgLysSerValPhe 454  
Db 1320 ACTCTAGTGGTGTGTGATGATGAGCTGAGAGAGTGTGAGCAATGAGAGTGGTGTTC 1379  
QY 455 AspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPheHis 474  
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Db 1440 ATGAATCATCTCTTCCAGGTTGGCCACAGAGTGAAGAGATGATGATGATGATGATGATG 1499

QY 494 SerLeuGlnAapPheCysAlaAlaLeuTyrTyrValLeuGluGluLeu--GluTleGlu 512  
Db 1500 AGCGTCGAGGATTTCTTGGCTGCTTATATATGTTTAAAGAGGCTGGAGAAATGGAAAT 1559  
QY 513 ProAlaLeuCysProLeuTyrValGluTyrThrIlysArgSerMetGluLeuGlnAla 532  
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QY 533 GlyPheHisIleHisSerLeuTyrMetIlysArgPheLeuPheGlyLeuValSerGluAsp 552  
Db 1614 GAC---GACACTGCGCTCTCGGAGATGAAGGTTTCTTATTTGGCTCATGAACAAGAT 1670  
QY 553 ValArgArgProLeuGluValLeuLeuGluGlyCysProValProLeuGluValIlyGlnIlys 572  
Db 1671 ATCTGAAGACTCTGGAGGTTCTGTTGAATATCCCGATGATCCAACTGTTCAGACAGAG 1730  
QY 573 LeuLeuHisTyrValSerLeuLeuGluGlyGlnGlnProAlaAlaThrThrProGlyAspThr 592  
Db 1731 CTCCAACACTGGGCTCTCTCTATAGCTCAGAGGTCATGGACACAGCCCAATGAGACAC 1790  
QY 593 LeuAspAlaPheHisCysLeuPheGluThrGlnAspIlysgluPheValArgLeuAlaLeu 612  
Db 1791 CTGATGCTCTTCTATGTCCTATTTGAGTCTCAGAGTGAAGAGTTGTTGGCGGGGCTCTC 1850  
QY 613 AsnSerPheGlnGluValTyrLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSer 632  
Db 1851 AAACGCTTCCAAAGAGTGTGCTGCTGATTAACCAAGAGTGAAGCTTGAAGGTCCTTCC 1910  
QY 633 PheCysLeuGlnHisCysProTyrLeuAspIlyIleArgValAspValIlyGlyIlePhe 652  
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QY 653 ProArgAspGluSerAlaGluAlaCysProValValProLeuTyr--MetArgAspIly 671  
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QY 712 LysAlaArgHisProThrCysAlaIleGlnThrLeuMetPheArgAsnAlaGlnIleThr 731  
Db 2151 GAGCTGGGGAATCAGTCTCGCAAGATACAGAAAGCTTAAAGAGTGCAGAGTATG 2210  
QY 732 ProGlyValGlnHisLeuTyrArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsn 751  
Db 2211 TCTGGCTCGAAACATCTCTGAGAGCTCTTTTGTAGCAATCAAACTTAAGTACTCAT 2270  
QY 752 LeuGlyGlyThrHisIleLeuGluGluAspValArgMetAlaCysGluAlaLeuIlyHis 771  
Db 2271 CTAGGAAACATCCCATGAGATGATACATGAAGTATGAGCTCGAAGCCCTGAACAT 2330  
QY 772 ProIlyCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyr 791  
Db 2331 CCAAGTCTCCCGAGAGACTCTGAGGTGATTCCTGTAGTTAACATCATGTTAT 2390  
QY 792 LeuIlyIleSerGlnIleLeuThrThrSerProSerLeuIlySerLeuSerLeuAlaGly 811  
Db 2391 GAGATGATCTCAGAGCTCTTATTTCAACSCAAGGCTAAAGTGTCTCAGCTGCGCCAA 2450  
QY 812 AsnIlyValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCys 831  
Db 2451 AATGAGGGAGAGTAAAGATGATATCCCTGGAGATGCTTGAAGTCAATGCT 2510  
QY 832 AlaLeuGlnIlyLeuGlnIleLeuGlnAspCysGlyIleThrAlaThrGlyCysGlnSerIle 851  
Db 2511 CTACTGCAAAAGTGTATCTGAGACACTGTGGCTCAGACACTGCGAGTGCACCTTCTG 2570  
QY 852 AlaSerAlaLeuValSerAsnArgSerLeuThrHisIleCysIleuSerAsnSerLeu 871

Db 2571 GTCTACGCTCTTTTCAACACAGAACTTGAACACTGTGCTGTCAACACAGCTG 2630  
QY 872 GlyAsnGluGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGln 891  
Db 2631 GGGAGTGAAGAGTGAAGAGCTGTGTCACTGCTGAGAAATCCAGAAATGTGCTCTCAG 2690  
QY 892 ArgLeuMetLeuGlnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAla 911  
Db 2691 CGGCTGATGATCATCTCAACATTTAGATGATGATCTTATGCTTCTCGCAATAGA 2750  
QY 912 LeuMetGlyAsnSerTyrLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsn 931  
Db 2751 CTTCGAAACACACAAAGCTGACCTGAGCTGACATGAACAGCCCGTGAAGGGAGTGT 2810  
QY 932 GlyValIlySerLeuLeuCysGluValMetArgGluProSerCysHisIleGlnAspLeuGln 951  
Db 2811 GCATGAAGTCACTGCTGTGAAGCTTAAAGAACTTACTTGTATACCTTCAAGAACTGGA 2870  
QY 952 LeuValIlyCysHisIleThrAlaAlaCysCysGluSerLeuSerCysValIleSerArg 971  
Db 2871 CTAGTGAAGTGCACAACTCAGACAGAACTGCTGCGAGGACCTGCTGTATGATCACAAC 2930  
QY 972 SerArgHisLeuIlySerLeuAspLeuThrAspAsnAlaLeuGluIlyAspGlyValAla 991  
Db 2931 ACCAAGACTTAAAGATTTGGATCTGTGTAACACGCTGGGTGTCAAAGAGTATA 2990  
QY 992 AlaLeuCysGluGlyLeuIlyAsnSerValLeuThrArgLeuGlyLeuIlyAla 1011  
Db 2991 ACCCTGTGTAAGGAGCTGAAGCAAGTACAGACTCCCTGAGAGACTGTGGGTTGGGGCA 3050  
QY 1012 CysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysValAsnArgHis 1031  
Db 3051 TGTAAGTGATCTTCAATTTCTGTGAAGCAATGTGCATGTGCAATCTGTCAACCTTCAC 3110  
QY 1032 LeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProIlysgluMetMetIlyLeuCys 1051  
Db 3111 CTGAACGCTTAACTGGGAGAAATGACTTCACTGATCAGTGGGAGATGTGAAGCTGTGC 3170  
QY 1052 SerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTyrIlyStrpGlnTyr 1071  
Db 3171 TCTGCTTCAATGCTGCTGTCTTAACTGTGGGATATTTGGCTGTGAAGCAGAACTAC 3230  
QY 1072 ProValGlnIleArgIlyLeuLeuGluGluValGlnLeuLeuIlyProArgValValIle 1091  
Db 3231 TATCCCGAGTGAAGAAACAGCTGAGAGAGTGAAGTTGATCAAGCCCAAGTGTAT 3290  
QY 1092 AspGlySerThrHisSerPheAspGluAspAspArgHis 1104  
Db 3291 GATGATGATTGTATGCTGATGATGAAGATGACCGAAG 3329  
  
RESULT 11  
US-10-677-943--5  
Sequence 5, Application US/10677943  
Publication No. US20040072297A1  
GENERAL INFORMATION:  
APPLICANT: The Government of the United States of America as  
APPLICANT: Represented by the Secretary of the Department of Health and  
APPLICANT: Human Services  
APPLICANT: Nelson, Lawrence  
TITLE OF INVENTION: Human Gene Critical to Fertility  
FILE REFERENCE: 4239-64790  
CURRENT APPLICATION NUMBER: US/10/677,943  
CURRENT FILING DATE: 2003-10-01  
PRIORITY APPLICATION NUMBER: 60/241,510  
PRIORITY FILING DATE: 2000-10-18  
PRIORITY APPLICATION NUMBER: PCT/US02/09776  
PRIORITY FILING DATE: 2002-03-29  
PRIORITY APPLICATION NUMBER: PCT/US01/10981  
PRIORITY FILING DATE: 2001-04-04  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.2

SRQ ID NO 5  
 LENGTH: 3447  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-10-677-943-5

## Alignment Scores:

Score:	8.76e-276	Length:	3447
Percent Similarity:	2688.00	Matches:	554
Best Local Similarity:	66.49%	Conservative:	186
Query Match:	49.78%	Mismatches:	293
	38.00%	Indels:	81
		Gaps:	11

US-10-066-521-6 (1-1344) x US-10-677-943-5 (1-3447)

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 Db 163 CAATGGCTCTCCA-GAAAAAGACAGTAAGCAATCTGMAAGCACTGGATGGAGAG 221  
 QY 35 LysLysSerSerGluSerThrThrCysSerLysPheGlnPheGlnLysLysLys 54  
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 Db 222 GAACAGAGATGAGAAAGCA- 242  
 QY 55 ValGluCysLeuAlaLeuLeuLeuHISgluTyrTyrGluAlaSerLeuAlaTrpAlaThr 74  
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 Db 242 ----- 242  
 QY 75 SerLysSerLysPheGluAsnMetAsnLeuLysThrLysSerGluLysAlaArgAsp 94  
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 Db 243 ---ATGTCCTCTTCAGAAATGTCAGTAGACCAATCTGMAAGCACTGGATGGAGAG 299  
 QY 95 MetLysLysLysSerGln- 100  
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 Db 300 GTGAAACAGGCGTCAGAAAGAAATGACTCTCCAGAAACGACAGTAATCAATCCAG 359  
 QY 101 -----AlaMetGluGlnGluGluAlaThrAlaAlaGluThrGluGluGln 115  
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 Db 360 AAAAGACCAAGACCAAGACAGACAGACATCAAGAACTTCAATCTAAGAGAGAGAT 419  
 QY 116 GluLysSerGlnAlaMetGluGlnGluGluAlaThrAlaAlaGluThrGluGlnGlu 135  
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 Db 420 GAAGTACAGAGGCA- 443  
 QY 136 HisGluLysAspThrTrpAspTyrLysSerHisValMetThrLysPheAlaGluGlu 155  
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 Db 444 AATGAGGTGACTTACAGAGCTACAGAGCCCATGTGATGCTAAGTTGACACAGAGTGG 503  
 QY 156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175  
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 Db 504 GATCTACAC- 542  
 QY 176 GluLysPheAspSerAspArgTrpGluLysPheArgProArgThrValLeuLeuHisGluLys 195  
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 Db 543 GATGCTTTTAAACATACAGAAACCTTCAGGCTCACACATTAATCTCATGAGAGAG 602  
 QY 196 SerGluLysGluLysSerAlaLeuAlaArgArgLysValLeuCysTrpAlaGlnGluLys 215  
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 Db 603 CCAGAGAGTTGGAGAGTCAAGCTTGGCCAGAGATATTTCTTGGCTGGGACAGGGTAA 662  
 QY 216 LeuTyrGlnGluMetPheSerTyrValPhePheLeuProValArgGluMetGluArgLys 235  
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 Db 663 CTCTTCGAAAAAG- 719  
 QY 236 LysGluSerSerValThrGluPheLysSerArgGluTrpProAspSerGlnAlaProVal 255  
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 Db 720 GAGAGAGACAGTTGGACAGCTGATCTCAAGAGGTCCAGACTCTCGGAGATCTAATG 779  
 QY 256 ThrGluLysMetSerArgProGluLysLeuLeuPheLysLysGluLysPheAspLeu 275  
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 Db 780 ACAAGATCATGTCTCCACAGAAAGACTCTGTGTTCATAGAGGTCTGATGATATG 839  
 QY 276 GlySerValLeu---AsnAsnAspThrLysLeuCysLysAspTrpAlaGluLysGlnPro 294

Db 840 GACTCTGCTCCCAACATGATGATATGACACTATCCAGAGACTGGAGAGTAAACGCC 899  
 QY 295 ProPheThrLeuLysSerLeuLeuArgLysValLeuLeuProGlnSerPheLeuLys 314  
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 Db 900 ATATACATCTGATGACGCTCTGAGAGAGCTCTTACCTCAAGTCTCTTCTCATC 959  
 QY 315 ValThrValArgAspValGluThrGluLysLysSerGluValValSerProArgTyr 334  
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 Db 960 ATTACACACAGAAACACAGGCTTAGAAAACTCAAGTCAATAGTGTGTCTCCCTCAT 1019  
 QY 335 LeuLeuValArgGluLysSerGluGlnArgLysLysLeuLeuLeuArgGluLys 354  
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 Db 1020 ATACTGTTGAAGACTGTCTGATCAAGAGATCTCAGTGTCTGAGAAACATCTCC 1079  
 QY 355 GlyLysLysGlnLysThrGlnGluLysArgAlaLeuMetAsnAsnArgGluLeuLys 374  
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 Db 1080 AATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139  
 QY 375 GlnCysGlnValProAlaValGluSerLeuLysCysValAlaLeuGlnLeuGlnAsp 394  
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 Db 1140 CAATGCCAGGCCCTCTGCTGTCTCTGCTGTCTGTGAGGCTCTACAGCTACAGAGAA 1199  
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 Db 1200 CTGGGAAAGAGATGACCTTACCTGAGCACTCTCAGCGGTTGTATGCCAGTTGGTG 1259  
 QY 415 PheHisGlnLeuThrProArgGluValValArgArgCysLeuAsnLeuGluLysVal 434  
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 Db 1260 TTTTCCAGCTCCTCACTTGAAGAAAGGCTTCCAGAGCGCTCTCAGCTCAGAGAAACAGTT 1319  
 QY 435 ValLeuLysArgPheCysArgMetAlaValGluGluValTrpAsnArgLysSerValPhe 454  
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 Db 1320 ACTTACGCGGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1379  
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 Db 1380 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1439  
 QY 475 MetAsnLysLeuLeuProAspSerHis---CysGluGluTyrTyrThrPhePheHisLeu 493  
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 Db 1440 ATGAACATCTCTTCCAGAGTGGCCACAAAGTACAGTGTATGATTTCTCCACCTC 1499  
 QY 494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGlnGluLys---GluLysGln 512  
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 Db 1500 AGCTGCGAGATTTCTTGTGCTGCTTATATATGTTTAAAGGCTGAGAGATTCAGAT 1559  
 QY 513 ProAlaLeuCysProLeuTyrValGluLysThrLysArgSerMetGluLeuLysGlnAla 532  
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 Db 1560 CAGCATTTTTC-----TTCAATTGAAACCAAGAGAGCATCAGAGGTGAAGAGACT 1613  
 QY 533 GlyPheHisLysSerLeuTrpMetLysArgPheLeuPheGluLysValSerGluAsp 552  
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 Db 1614 GAC---GACACTCCCTCTCTGGAGTGAAGGTTTCTTATTTGGCTCATCAACAGAGAT 1670  
 QY 553 ValArgArgProLeuGluValLeuLeuGluCysArgProValProLeuGluValLysGlnLys 572  
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 Db 1671 ATCTTGAAGACTCTGAGAGTCTGTGATGATATCCCGATTCACACTGTGAGAGAGAG 1730  
 QY 573 LeuLeuHisTrpValSerLeuLeuGluGlnGlnProAsnAlaThrThrProGluLysAspThr 592  
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 Db 1731 CTCAACACACTGGGCTCTCTGATAGCTCAGAGAGTCAATGSCACACAGCCCAATGAGACCC 1790  
 QY 593 LeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeu 612  
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 Db 1791 CTGATGCTCTTCTATTTGCTATTTGAGTCTCAGATGATGAAGGTTGTTGGCGGCGCTCTC 1850  
 QY 613 AsnSerPheGlnGluValTrpLeuProLysGlnGlnLeuAsnLeuAspLeuLysLysSer 632  
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 Db 1851 AAAGCTTCCAAAGAGTGGCTCTGATTAACCAAGAGATGAGCTTGAAGCTCTCTCC 1910  
 QY 633 PheCysLeuGlnHisCysProTyrLeuArgLysLysLeuValAspValLysGluLysPhe 652  
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Db 1911 TACTGTCTCAAGCACTGTCAAGACTTGAAAGCAATCCGGTGGATATTCAGAGACCTCTC 1970
Qy 653 ProArgAspGluSerAlaGluAlaCysProValValProLeuTrp---MetArgAspLys 671
Db 1971 TCGAGTAGTAATTAATCTCGAGCTGTGCCCTGTGTGTACTGTCTCAGAGACCAACATGTAAG 2030
Qy 672 ThrLeuIleGluGluGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeu 691
Db 2031 CCCCTCCATGAGTAGGTGGTGGGAAACTTGTGCTGTGCTGGCAGCTCCGGAACTGG 2090
Qy 692 ArgGluLeuAspLeuGlySerSerIleLeuThrGluAlaMetLeuThrCysAla 711
Db 2091 AAGAGCTGGACTTGGGCGACAGCATCTGTAGTCAACGGGCAATGAAATACTGTGCTC 2150
Qy 712 LysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAspAlaGlnIleThr 731
Db 2151 GAGCTGCGGAATCAATCTCGCAGAAATACAGAAAGTGAAGTTTAAGAGCAGAGTAGTG 2210
Qy 732 ProGlyValGlnHisLeuThrTrpArgIleValMetAlaAspArgAspLeuArgSerLeuAsn 751
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Qy 752 LeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHis 771
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Qy 792 LeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuLeuAlaGly 811
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Qy 812 AsnLysValIleTrpAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCys 831
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Qy 832 AlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThrGlyCysGlnSerLeu 851
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Qy 852 AlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeu 871
Db 2571 GTCTCAGGCTTTTTCAGAACACCACTTGACACACCTGTGCTGTCAAAACACAGCTGT 2630
Qy 872 GlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGln 891
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Qy 892 ArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAla 911
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Qy 912 LeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsn 931
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Qy 952 LeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerArg 971
Db 2871 CTAGTGAAGCTGCAACTCACACAGAACTGTGCGAGACCTGGCTGTATGATACACACA 2930
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RESULT 12
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US200400286941
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US/10/399,443
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-1

Alignment Scores:
Pred. No.: 1,46e-203 Length: 1157
Score: 2005.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.34% Indels: 0
Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-1 (1-1157)
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Db 1 CAAGCTCCGGTGAAGGAGATCATGTCCGACCAAGAAAGCGCTGTGTTCATCATATGAGCGT 60
Qy 272 PheAspAspLeuGlySerValIleuAsnAsnAspThrLysLeuCysLysAspTrpAlaGlu 291
Db 61 TTCATGACTCTGGGCTGTCTCTCAACAATGACCAAGAGCTGTGCAGAAAGACTGGGCTGAG 120
Qy 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValIleLeuProGluSer 311
Db 121 AAGCAGCTCCGTTCACTCATACGCAAGTGTGTGAGGAAGTCCGTGCTCCGAGATCC 180
Qy 312 PheLeuIleValIleThrValArgAspValGlyThrGluLysLeuLysSerGluValValSer 331
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Db 181 TTCCTGATCGTACCGTACAGAGCTGGGCAAGAAAGTCAAGTCAAGGCTGCTCT 240  
 Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGlnGlnGlnIleIleLeuLeuGlu 351  
 Db 241 CCCCGTACCTGTTAGTAAAGAAATCTCCGGGAAACAAAGATCCATGCTCTTGAAG 300  
 Qy 352 ArgGlyIleGlyGlnIleGlnIleThrGlnGlnIleuAgaIleIleMetAsnAsnArgGlu 371  
 Db 301 CGCGGAGTGGTGAAGCATCAAGAAAGCAAGAGGTTGCGGTGATATGAACACCTGAG 360  
 Qy 372 LeuLeuArgGlnGlyGlnValProAlaValSerIleIleCysValAlaLeuGlnLeu 391  
 Db 361 CTGCTGCACAGTGCAGAGTCCCGCGGTGCTCTCATCTGGGCTGACGCTG 420  
 Qy 392 GlnAspValValGlyGlnSerValAlaProPheAsnGlnThrLeuThrGlyLeuIleAla 411  
 Db 421 CAGAGCGTGGGGGAGAGCGTCCGCTTCAACCAAGCGTCAAGGCTGCACGCC 480  
 Qy 412 AlaPheValPheIleGlnLeuThrProArgGlyValAlaArgArgCysLeuAsnLeuGlu 431  
 Db 481 GCTTTTGTTTCATCAGCTCAACCCCTGAGGCGTGGTCCGGCGCTGTCTCATCTGAG 540  
 Qy 432 GlnArgValValLeuLysArgPheCysArgMetAlaValGlnGlyValTyrAsnArgLys 451  
 Db 541 GAAAGAGTGTCTGAAAGCGCTTCTGCGGTATGGCTGGAGGAGTGTGAATAGAG 600  
 Qy 452 SerValPheArgGlyAspAspLeuMetValGlnGlyLeuGlnGlySerGlnLeuArgAla 471  
 Db 601 TCAGTGTGTGACGGTGAACCTCATGTGTTCAAGACATCGGGAGTCAAGTCCGTCT 660  
 Qy 472 LeuPheIleMetAsnIleLeuLeuProAspSerHisCysGlnGlnTyrTyrThrPhePhe 491  
 Db 661 CTGTTTCAAGAACATCTTCTCCCAAGACCACTGTAGAGATCTCAACCTTCTTC 720  
 Qy 492 HisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGlnGlyLeuGlnIle 511  
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 Qy 512 GlnProAlaLeuCysProLeuTyrValGlnLysThrLysArgSerMetGlnLeuLysGln 531  
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 Qy 532 AlaGlyPheHisIleHisSerLeuThrMetLysArgPheLeuPheGlyLeuValSerGlu 551  
 Db 841 GAGGCTTCCATATCCATCGCTTGTGAAGAGCTTCTGTGTGGCTGTGAGCCAA 900  
 Qy 552 AspValArgArgProLeuGlnValIleLeuGlnGlyCysProValProLeuGlyValLysGln 571  
 Db 901 GACGTAAAGAGGCACTGAGGCTCTGCTGGGCTGTCCGTTCCCTGGGGGTGAAGCAG 960  
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 Db 961 AAGCTTGCACATGGGTCTCTGTGGGTGAGCAGCCTTAATGCCACCAACCCAGAGAAC 1020  
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 Db 1021 ACCGTGAAGCGCTTCACTGTCTTTCAGACTCAAGCAAAAGATTTGTGCTTGCA 1080  
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 Db 1081 TTTAAACAGCTTCCAAGAGTGTGCTTCCGATTAACCAAGACCTGACTTGAATGACATCT 1140  
 Qy 632 SerPheCysLeuGln 636  
 Db 1141 TCCTTCTGCTCAG 1155  
 RESULT 13  
 US-10-677-943-1  
 ; Sequence 1, Application US/10677943  
 ; Publication No. US20040072297A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Government of the United States of America as  
 ; represented by the Secretary of the Department of Health and

; APPLICANT: Human Services  
 ; APPLICANT: Nelson, Lawrence  
 ; APPLICANT: Tong, Zhi-Bin  
 ; TITLE OF INVENTION: Human Gene Critical to Fertility  
 ; FILE REFERENCE: 4239-64730  
 ; CURRENT APPLICATION NUMBER: US/10/677,943  
 ; PRIOR FILING DATE: 2003-10-01  
 ; PRIOR APPLICATION NUMBER: 60/241,510  
 ; PRIOR FILING DATE: 2000-10-18  
 ; PRIOR APPLICATION NUMBER: PCT/US02/09776  
 ; PRIOR FILING DATE: 2002-03-29  
 ; PRIOR APPLICATION NUMBER: PCT/US01/10981  
 ; PRIOR FILING DATE: 2001-04-04  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 1157  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-677-943-1  
 Alignment Scores:  
 Pred. No.: 1,46e-203 Length: 1157  
 Score: 2005.00 Matches: 385  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 28.34% Indels: 0  
 DB: 17 Gaps: 0  
 US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)  
 Qy 252 GlnAspProValThrGlnIleMetSerArgProGlnArgLeuPheIleAspGly 271  
 Db 1 CAGGCTCGGTGAGAGATATGTCCTCCAGACAAAGAGCTGTGTATCATATGACGT 60  
 Qy 272 PheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCysLysAspTyrAlaGlu 291  
 Db 61 TTCATATGACTGGGCTGTCTGTCTCAACATATGACAAAGCTCTGCAAGAGCTGAG 120  
 Qy 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSer 311  
 Db 121 AAGCAGCTCGGTTCACCTCATACGAGTCTGCTGAGAAAGTCTCTCTGAGTCC 180  
 Qy 312 PheLeuIleValThrValArgAspValGlyThrGlnLysLeuLysSerGlnValAlaSer 331  
 Db 181 TTCCTGATCGTACCGTCAAGAGCTGGGCAAGAGAACTCAAGTCAAGGCTGTCT 240  
 Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGlnGlnIleIleLeuLeuGlu 351  
 Db 241 CCCCGTACCTGTTAGTAAAGAAATCCCGGGAAACAAAGATCCATGCTCTTGAAG 300  
 Qy 352 ArgGlyIleGlyGlnIleGlnIleThrGlnGlnIleuAgaIleIleMetAsnAsnArgGlu 371  
 Db 301 CGCGGAGTGGTGAAGCATCAAGAAAGCAAGAGGTTGCGGTGATATGAACACCTGAG 360  
 Qy 372 LeuLeuArgGlnGlyGlnValProAlaValSerIleIleCysValAlaLeuGlnLeu 391  
 Db 361 CTGCTGCACAGTGCAGAGTCCCGCGGTGCTCTCATCTGGGCTGACGCTG 420  
 Qy 392 GlnAspValValGlyGlnSerValAlaProPheAsnGlnThrLeuThrGlyLeuIleAla 411  
 Db 421 CAGAGCGTGGGGGAGAGCGTCCGCTTCAACCAAGCGTCAAGGCTGCACGCC 480  
 Qy 412 AlaPheValPheIleGlnLeuThrProArgGlyValAlaArgArgCysLeuAsnLeuGlu 431  
 Db 481 GCTTTTGTTTCATCAGCTCAACCCCTGAGGCGTGGTCCGGCGCTGTCTCATCTGAG 540  
 Qy 432 GlnArgValValLeuLysArgPheCysArgMetAlaValGlnGlyValTyrAsnArgLys 451  
 Db 541 GAAAGAGTGTCTGAAAGCGCTTCTGCGGTATGGCTGGAGGAGTGTGAATAGAG 600  
 Qy 452 SerValPheArgGlyAspAspLeuMetValGlnGlyLeuGlnGlySerGlnLeuArgAla 471



Db	601	TCAGGTTGACGGTGAACAGCACTCAATGTTCAAGACTCGGGGAGTCTGACCTCGTCT	660
Qy	472	LeuphehIsmetAsmIleuleuProapSerhiCyeglulnYrYrThrPhephe	491
Db	661	CTGTTTCACATGAACATCTCTTCCACAGCACCCACTGAGAGGATCAACCTTCTTC	720
Qy	492	HisleuseriLeuGlnAspPheCysAlaIaleuYrYrValIleuInIleuInIle	511
Db	721	CACCTCAAGTCTCCAGGACTTCGTGCGGCTGTACTAGTGTGAAGGAGCTGGAAATC	780
Qy	512	GluProAlaleuCyapProleuYrValGluYrThrIlyArgSerMetGluIleuYsgin	531
Db	781	GAGCAGGCTCTCGCCCTCTGTACGTTGAGAAACAAAGAGGCCATGAGGCTTTAAACAG	840
Qy	532	AlaGlyPhehIaIleHiseriLeuTPMetIlyArgPheLeuPheIlyleuValSeriGlu	551
Db	841	GAGGCTTCATATCACTACGCTTGGAATGAAGCGTTCTGTGGCTCGGACCGAA	900
Qy	552	AspValArgArgProleuGluValIleuIleuGlyCyapProValProleuGlyValIlysgin	571
Db	901	GACGTAAAGAGGCCACTGGAAGGTCGTGGGCTGTCGCCGTTCCCTGGGGGGTGAAGCAG	960
Qy	572	IlySleLeuLeuHisITrValSeriLeuIleuGlyGlnGlnProAsnAlaThrThrProGlyAsp	591
Db	961	AAGCTTCGACACTGGGTCTCTCTGTGGGTACAGCACTTAATGCCACACCCAGAGAGAC	1022
Qy	592	ThrIleuAspAlaPhehIeCySleuPheGluThrGlnAspIlyGluPheValArgIleuAla	611
Db	1021	AACCTGGAAGCGCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTGTTCGCTTGGA	1082
Qy	612	LeuAsnSerPheGlnGluValITrleuProIleAsnGlnAsnLeuAspLeuIleAlaSer	631
Db	1081	TTAAACAGCTTCCAGAGAGTGTGGCTTCGATTAACAGAACTGACTTGATGATCATCT	1142
Qy	632	SerPheCySleuGln	636
Db	1141	TCCTTCTGCTCCAG	1155
RESULT 14			
US-10-794-342-2			
: Sequence 2, Application US//10794342			
: Publication No. US20040253615A1			
: GENERAL INFORMATION:			
: APPLICANT: Inohara, Naohiro			
: APPLICANT: Nunez, Gabriel			
: TITLE OF INVENTION: NOD Nucleic Acids and Polypeptides			
: FILE REFERENCE: UM-08922			
: CURRENT APPLICATION NUMBER: US/10/794,342			
: CURRENT FILING DATE: 2004-03-05			
: NUMBER OF SEQ ID NOS: 22			
: SOFTWARE: PatentIn version 3.2			
: SEQ ID NO 2			
: LENGTH: 3521			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-10-794-342-2			
Alignment Scores:			
Pred. No.:			
Score:	5,45e-190	Length:	3521
Percent Similarity:	1885.50	Matches:	422
Best Similarity:	56.65%	Conservative:	208
Best Local Similarity:	37.95%	Mismatches:	443
Query Match:	26.65%	Indels:	39
DB:	18	Gaps:	13

Dd	88	AAACAAGAGAAATTAAATACATTCAG---TTATTCTTAAGAGAGACATGGAACCTGAG	144
Oy	42	ThrCysSerIleProGlnPheGluIleGluSerAlaSerValGluCysLeuAlaLeuLeu	61
Dd	145	CATGGCCCTGACACCCTGGATGAAGTGAAGAGCGACGCGGAGAGACCTGGCCAAATTGG	204
Oy	62	LeuHISGLUTYRTYRGLYAlaSerLeuAlaThrAlaThrSerIleSerIlePheGluSer	81
Dd	205	ATGAAGAAATTTATTCAGAGAGAGAAACCCTGGAGGTGCTCTCAAAATCTTTGGCAG	264
Oy	82	MetAlaLeuArgThrLeuSerGluIleValAlaArgAspAspMetCysGluIleSerGlnAla	101
Dd	265	ATGAACCTGGAAGATCTGTGTGAGAGAGCGAAAGAGATCACTGTGTGGCCCAAGACT	324
Oy	102	MetGluGlnGluGlyAlaThrAlaAlaGluThrGluGlnGlnGlyIleSerGlnAlaMet	121
Dd	325	ATAGACACCAATGATGCGCAAGCTGGAGAGACACAGAA-----	363
Oy	122	GluGlnGluGlyAlaThrAlaAlaGluThrGluGlnGlnGlyIleSerGlnAlaMet	141
Dd	364	GATCAGGAGGAGCATGCTG-----GGTATGGAACA	393
Oy	142	AspTYRLeuSerHisValMetThrCysPheAlaGluGluGluAlaAspValArgArgSerPhe	161
Dd	394	GAATTCAGAAATTAAGATTAAGAAATAATTTGCATCACTGGGAC---AAGAAGCTTTG	450
Oy	162	GluSerThrAlaAlaAspTrp-----ProGluMetGlnThrLeuAla	175
Dd	451	GCTGAAAGCCTGAAGATTTCCATCATGGAATTCAGAGAAAGATAGAATACTTTGGAA	510
Oy	176	GlyAlaPheAspSerAsp---ArgTrpGlyPheArgProArgThrValValLeuHISGLY	194
Dd	511	CACCTGTTCCATGTGGAGTGCAGAAACCGGTGCACAGCCAGATCGTGCTTCACAGGA	570
Oy	195	LysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValIleuCysTrpAlaGlnGly	214
Dd	571	GCTGCTGAGATTGGGAAACCAACTTGGTGAAAGAGCAATGTGATGGGACAGAGGC	630
Oy	215	GlyLeuTYRGLYMetPheSerTYRValPhePheLeuProValArgGluMetGlnArg	234
Dd	631	AGTCTTACACGACAGAGGTTTAAGATGTTTTTATCTCAATGGGAGAAATTAAACAG	690
Oy	235	LysIleGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaPro	254
Dd	691	CTGAAGAGAGAACTTTGCTCAATGTATTCAAAGACCTGGCCACGACAGAAAGCCCC	750
Oy	255	ValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspArg	274
Dd	751	ATTGAGAAATCAATGTACACGCCAAAGTACCTCTGTGTTATTATTGACAGTTTCATGAA	810
Oy	275	LeuGlySerValIleuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGluIleGln	293
Dd	811	CTGAACCTTGGCTTTGAAGAACCCTGAGTTTGACCTGTGCAAGACCTGACCAAGAAC	870
Oy	294	ProProPheThrLeuIleArgSerLeuLeuArgLysValIleLeuLeuProGluSerPheLeu	313
Dd	871	CCAGTGTCTTCTCATAGATGATGATTTGCTGAGGAAGATGATCTCCCTGAGGCACTTTA	930
Oy	314	IleValThrValArgAspValGlyThrGluLysLysSerGluValValSerProArg	333
Dd	931	TTGGTGAACAAAGACTCAACAATCTTAAGAGACTTAAGACGCTGTGTAAAGATACCAT	990
Oy	334	TyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisIleLeuLeuGluGluArgGly	353
Dd	991	TATGTAGAGCTACAGAAATGTCGAGAGATCCAAAGAGAGATATTTACCAAGTTTTT	1050
Oy	354	IleGlyGluHISGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeu	373
Dd	1051	GAAGATTAAGAGGTGGCCATGAAGATATTCATTCACATAAAGCAATGAGATGCTGTTT	1110
Oy	374	AspGlnCysGlnValProAlaValGlySerIleLeuCysValAlaIleGlnLeuGlnAsp	393
Dd	1111	AGCATGTGGCAAGTCCCTTATGTGTGTGTGGGCGCTGTGTATTTGTCTGAAGACGAATAATG	1170

Qy 394 ValValGlyGlySerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPhe 413  
Db 1171 GAGAGGGTGGTGGATGTCATTCAGTCCGACCAACACAGCTCTGTTAACTGTCAT 1230  
Qy 414 ValPheHisGlnLeuThrProArgGlyValValAlaGlyGlySerLeuAsnLeuGlnArg 433  
Db 1231 ATTCTTACCTGTTCCACCA-----GTAGATGAGGCTCTCCATGCTCCACCAACA 1284  
Qy 434 ValValLeuValArgPheCysArgMetAlaValGlnGlyValTyrAsnArgGlySerVal 453  
Db 1285 GCCCAGTGAAGAAAGCTGTGCCAGTCCGTCCCAAGAAATAGACATATGACTTAAGT 1344  
Qy 454 PheArgGlyAspArgPheLeuMetValGlnGlyLeuGlyGlySerGlnLeuArgAlaLeuPhe 473  
Db 1345 TTTTACAGAGAAATCTCAGAAAGCTTGCTTAATCTCATCTGATGCTCAAGTTTANG 1404  
Qy 474 HisMetAsnIleLeuLeuProArgSerHisCysGlnGlyTyrTyrThrPhePheHisLeu 493  
Db 1405 GACAGCAATATTATTACAGAAAGACAGAGATGAAACTGCTATGTGTCCACCACTT 1464  
Qy 494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValIleuGlnGly---LeuGlnIleGln 512  
Db 1465 CATGTCAGAGAGTTTTCAGACTATGTCTATATGTTGAAGGAGCTTGGAACCTGG 1524  
Qy 513 ProAlaLeuCysProLeuTyr-----ValGlnGlySerHisSerMetGlnLeuArg 530  
Db 1535 AACCTTCTGTCAGACCTTTGAAAGATTTGAAGTCACTTAATCTCAAGACCAAGTTATAA 1584  
Qy 531 GlnAlaGlyPheHisIleHisSerLeuThrMetIleValArgPheLeuPheGlyLeuValSer 550  
Db 1585 GACCC-----CATTTGACACAGATGAAGTCTTTTGTGGCTTTGAT 1632  
Qy 551 GlnArgValAlaGlyGlyProLeuGlnValLeuLeuGlyCysProValProLeuGlnValArg 570  
Db 1633 GAGAGTTCAGATAAACAACCTGAGAGGACTTTAACTGTAATCTCACTGAAGTTAA 1692  
Qy 571 GlnIleLeuLeuHisIleThrValSerLeuGlnGlnGlnProAsnAlaThrThrProGly 590  
Db 1693 TCAAAGTTCATTCAGATGATAGAGATTTAGAAACAAGTACTATCTCCATCAGACTG 1752  
Qy 591 AspThrLeuAspAlaPheHisCysLeuPheGlnThrGlnAspArgGlyPheValArgLeu 610  
Db 1753 GAATTTCTGAGTGTTCACGTCTGTATAGACTCAAGATTAAGCCTTTATAGCCAG 1812  
Qy 611 AlaLeuAsnSerPheGlnGlnValTyrLeuProIleAsnGlnAsnLeuAspIleAla 630  
Db 1813 GCAATGAGATGTTCCCAAGAGGTGCCATTAATTTGTGAGAAATACATTTGCTGTA 1872  
Qy 631 SerSerPheCysLeuGlnHisCysProTyrLeuArgGlyIleArgValAspValIleGly 650  
Db 1873 TCTTTCTTCTGCTTAAACACCTGCGGTGTTGCGAACATCAGGCTGTCTGTAACCTG 1932  
Qy 651 IlePheProArgAspGlySerAlaGlnAlaCysProValValProLeuThrPheArgAsp 670  
Db 1933 GTATTGGAAGAGATATTAAAAACAAGCTCCCA---ACTAACATTTGGAGATGTAT 1988  
Qy 671 LysThrLeuIleGlnGlnIleTyrGlnAspPheCysSerMetLeuGlyThrHisProHis 690  
Db 1990 CGC-----ATTACTCAGCTGTGGCAAGATCTCTGTTGCTTCATTAACAATGACAC 2043  
Qy 691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetIleThrLeuArg 710  
Db 2044 TTGAGAGATTTGAGACTGTACATCAGAACCTGTATATGACGCAATAGATATCTTGAT 2103  
Qy 711 AlaIleValArgHisIleProThrCysIleValIleGlnThrLeuMetPheArgAsnAlaGlnIle 730  
Db 2104 CATGACTAAGGACCAACTGTAATCTAACAAGCTAAGCTTGAATTTATCATCTTC 2163  
Qy 731 ThrProGlyValGlnHisLeuThrArgIleValMetAlaAsnArgAsnLeuArgSerLeu 750  
Db 2164 CCGTATGGTGTGACAGATATCTCTACTTCTTTGATTCATTAACAAGATCTGATGATCTT 2223

Qy 751 AsnLeuGlyGlyThrHisLeuLeuGlyGlnIleAspValAlaGlyMetAlaCysGlnAlaLeuArg 770  
Db 2224 GACCTTAAAGGAGATATAGGAGATATGAGATTAAGTATGCTGTGAGCCCTTGAAA 2283  
Qy 771 HisProArgCysLeuLeuGlnSerLeuArgLeuAspArgCysGlyLeuThrHisAlaCys 790  
Db 2284 CACCCAGAGTAAACATACAGACTCTCAGGCTGGAGATCTTGCAACCTTAAGCTATTTGT 2343  
Qy 791 TyrLeuValIleSerGlnIleLeuThrThrSerProSerLeuArgSerLeuSerLeuAla 810  
Db 2344 TGTCTAATATATATCATAGCTCTATACAGAACCCAGACCTGATTTCTGATGTGCA 2403  
Qy 811 GlyAsnValThrArgGlnGlyValMetProLeuSerAspAlaLeuArgValSerGln 830  
Db 2404 ACCAATATCTGTTGATGATGAGAGTCACTTTGTGTGTGAGGCTTAAAGCATCCAAAG 2463  
Qy 831 CysAlaLeuGlnIleLeuGlnIleLeuGlnAspArgGlyIleThrAlaThrGlyCysGlnSer 850  
Db 2464 TGTATCTTAGAGAGCTGTCTTAGAAAGCTGTGTCTCAGAGAGCTGCTGTGATAT 2523  
Qy 851 LeuAlaSerAlaLeuValSerAspArgSerLeuThrHisLeuCysLeuSerAsnAsnSer 870  
Db 2524 CTTCCTTGGCTCTCATGACATTAAGACCTGACATTCATTTGTGCTTGACAGACATGTC 2583  
Qy 871 LeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCysSerLeu 890  
Db 2584 TTGGGTATGATGAGATTAAGCTTATAGTATGATGATGATGATGATGATGATGATGAT 2643  
Qy 891 GlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeu 910  
Db 2644 AAGAGCTTGTGCTGAGGCTGTGCTGATTTCACTTCACTTCACTTCACTTCACTTCACT 2703  
Qy 911 AlaLeuMetGlnValSerThrLeuThrHisIleLeuSerLeuSerMetAsnProValGlnArg 930  
Db 2704 TCTCTTCTTCAACAACAAGCTTACGATGATGATGATGATGATGATGATGATGATGAT 2763  
Qy 931 AsnGlyValIleValLeuLeuCysGlnValMetArgGlnProSerCysHisLeuGlnAspLeu 950  
Db 2764 AATGAGAGAGCTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2823  
Qy 951 GlnLeuValIleValCysHisLeuThrAlaAlaCysCysGlnSerLeuSerCysValIleSer 970  
Db 2824 GAATGATGAGGCTGTGCTTCAATGCAATGATGATGATGATGATGATGATGATGATGAT 2883  
Qy 971 ArgSerArgHisIleLeuSerLeuAspLeuThrAspAsnAlaLeuGlyAspGlyVal 990  
Db 2884 AATAACCCAAACCTGAGAGGCTTGACCTTGGAACAACGATTTGACAGATGATGAGATG 2943  
Qy 991 AlaAlaLeuCysGlnGlyLeuLeuGlnIleValAsnSerValLeuThrArgLeuGlyLeuArg 1010  
Db 2944 AAAATTTCTGTGATGCTTTTGAATATGCAAACTGTAACATTCACAGGCTGGGTTGAA 3003  
Qy 1011 AlaCysGlyLeuThrSerAspCysCysGlnAlaLeuSerLeuAlaLeuSerCysAsnArg 1030  
Db 3004 TACTGTGTTGATCATCTCTGCTGCAAGATCTCTCTGCTCTTATCTGCAACAA 3063  
Qy 1031 HisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProIleGlyMetMetIleLeu 1050  
Db 3064 AGACTGATTAAGAAATGAATACACAGAAATCTTAGAGATTAAGAAATGATGAAAGTTA 3123  
Qy 1051 CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuThrTyrProGln 1070  
Db 3124 TATTAAGCTTGAAGCTCTTAAGTAACTGAAGTTCTTAAGGTTGTGCAAGAGCA 3183  
Qy 1071 TyrProValGlnIleArgGlyLeuLeuGlnGlnValAlaGlnLeuLeuValProArgValAla 1090  
Db 3184 TTGATGAGAGAGCCAGAACTGCTGGAAGCTGGAAGTATGAGATTCACACTAATC 3243  
Qy 1091 IleAspGlySerThrHisSerPheAspGlnAspAsp 1102  
Db 3244 ATTAAGCCAGATGATTAATCATATATGAAAGAT 3279

RESULT 15



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Qy 540 TrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluVal 559
      ::::: ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1561 TTTTGGGGGTGTTTCTAACTGGCTTTAAATAAAGAAACAAGAAACTGGATCG 1620
Qy 560 LeuLeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeu 579
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1621 TTTTGGCTTCCAACTCTCCCAAGAGATAAAGCAGCAAAATTCACACAGTCTCCAGAGAGC 1680
Qy 580 LeuGlyGlnGlnProAspAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeu 599
      ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1681 TTAGGGAGCGTGGCAATCTCCAGGACAGGATGCTTGGCGATATTTTACTGCTGC 1740
Qy 600 PheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrp 619
      ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1741 TTTGAAGACAGATCTCGCTCTTGTGAAGACAGAGATGAACTCTCCAAAGACTAAC 1800
Qy 620 LeuProIleAsnGlnAsnLeuAspLeuIleAsnSerPheCysLeuGlnHisCysPro 639
      ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1801 TTTGATATTATGACAACTGGATCTGGTGTCTGCTACTGCTTAAATACTGCTCC 1860
Qy 640 TyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerIleGlu 659
      ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1861 AGCTTGAGAACTCTGTTTTCGTTCAAAATGCTTTAAGAAAGAGATGAACACACACC 1920
Qy 660 AlaCysProValProLeuThrMetArgAspLysThrLeuIleGluGlnTrpGlu 679
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1921 TCT-----ACGTGGATTAACCTCATC-----TGTTGGCAT 1953
Qy 680 AspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSer 699
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1954 CACATCTGCTCTGAGCTCACACACAGGAGCACTCAGAGAGCTCAGAGAGAGAGAGAGAG 2013
Qy 700 IleLeuThrGlnValGlnMetLysThrLeuCysValLysLeuArgHisProThrCysLys 719
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2014 ACCCTCAGCAGGAGCTGCTGTGACCTGTGTAAACAGCTGAGCACTCCAGCTGTGC 2073
Qy 720 IleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisIleLeuArg 739
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2074 CTTCAAGACTTGAATAATAATTAACCTTCTTCTTGGCCAGAGCTTCTGCTTTAG 2133
Qy 740 IleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisIleLeuArg 759
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2134 GTGCTCTTATCAAGCAGCACTTGAATAACCTGAGCTCACCTCAGCAAACTGTCTGT 2193
Qy 760 GluAspValArgMetAlaCysGluValLeuLysHisProLysCysLeuLeuGluSerLeu 779
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2194 GATGACATCAGGCTCCTCTGTGATGCTTGAATCAACCA----- 2232
Qy 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTrpLeuLysIleSerGlnIleLeuThr 799
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2232 ----- 2232
Qy 800 ThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyVal 819
      ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2233 -----GCAGGCAAC----- 2241
Qy 820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGlu 839
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2242 -----GTCAAGAGCTGACGCTGTGTA 2262
Qy 840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2263 AATTGTCACTCTCAACCATTTGATTTGATGAGCTTGTGGCTTTCAACCAACACACAG 2322
Qy 860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeu 879
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2323 AAGCTGACGTATCTGAATGATATCTGCAACAGTTA---GACACAGAGGCTGCCCTTTTG 2379
Qy 880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgMetLeuAsnGlnCysHis 899
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2380 TGTGAAGCCCTGTGACAGCCAGACAGGCTCTGTGATACCTGATGCTTGTCTGCAAC 2439

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Qy 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
      ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2440 CTCAAGCAGCAGCTGCTGGAAATACATCTCTCAAAATGCTTGGCTGAACAAGACGCTGGC 2499
Qy 920 HisLeuSerLeuSerMetAsnProValGlnLysAsnGlnValLysLeuLeuCysGluVal 939
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2500 TATCTAGACTCTCAGTGCCTCAATGTCTGAAGACAGAGGATGAAACTCTCTGCGAGGCC 2559
Qy 940 MetArgGluProSerCysHisIleGlnAspLeuGlnLeuValLysCysHisIleThrAla 959
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2560 TTGAACATCTCGAGCTGCTGCTGATTCATCTGTGTTGGTAAATGTTTATCATCTGCT 2619
Qy 960 AlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisIleLeuLysSerLeuAsp 979
      ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2620 GCTGGCTGTGAAGACTGCTGCTGCTGTATCAAGCATCAAACTGAAGATTCGTCAA 2679
Qy 980 LeuThrAspAsnAlaLeuGlyLysArgLysIleValAlaAlaLeuCysGlnGlyLeuLysGln 999
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2680 ATTGGGTGCATGAAATGAGATGTGGTGTGCAGCTGTGTGTCTGGGCTTCAGCGCAT 2739
Qy 1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCys 1019
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2740 ACGATTCGCCCTTAGAGATTCCTGGGTTGAAGATGTGGTTAACAGACACCTGCTGT 2799
Qy 1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisIleThrSerLeuAsnLeuValGln 1039
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2800 AAGATCTCGGCTGTCTTCACTGCAAGTGAAGACCTGCAGCAGCTCAACTGACCTTG 2859
Qy 1040 AsnAsnPheSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSer 1059
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2860 AACACTTGACCAACACAGGGGTGGTGTGTACTCTGTGAGGCCCTGAGACACCCAGAGTGT 2919
Qy 1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnIleProValGlnIleArgLysLeuLeu 1079
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2920 GCCCTGAGGTGCTGGCTGAGAAATGATTTTGAAGAAACCCAGAGCACTTGTG 2979
Qy 1080 GluGluValGlnLeuLysProArgValIleAsp----- 1092
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 2980 ACGGTGAAGAAAGAAATCTTAACCTGACCATCAAGATGACTGTGACAAATCACA 3039
Qy 1093 -----GlySerTrpHisSerPheAspGluAspAspArgHisLys 1105
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 3040 AGGTGAGATCTGATGTCGAGAACTCG----- 3069
Qy 1106 IleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGly 1125
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 3070 ---GCTGTACTCGAACACTGCAAGAGACAGGACTGGAC---CGTTACTTACATGAC 3123
Qy 1126 MetAsnProGluGlnLysLysArgValSerLeu 1136
      ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 3124 ACTGCACCCAGAGATACAAATCATGTGACACTC 3156

```

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 Job time : 1762 secs

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